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* * * * * * * * * * * * * STN Columbus * * * * * * * * * * * * * *
FILE 'HOME' ENTERED AT 17:34:33 ON 04 AUG 2004
=> FILE BIOSIS, CABA, CAPLUS, EMBASE, JAPIO, LIFESCI, MEDLINE, SCISEARCH, USPATFULL
=> e fraser claire m/au
E1          3   FRASER CIRA/AU
E2         21   FRASER CLAIRE/AU
E3        704 --> FRASER CLAIRE M/AU
E4          4   FRASER CLAIRE MARIE/AU
E5          1   FRASER CLARE/AU
E6          4   FRASER CLARE M/AU
E7          2   FRASER CLARENCE/AU
E8          4   FRASER CLARENCE F/AU
E9          1   FRASER CLARENCE L/AU
E10         2   FRASER CLARKE/AU
E11         1   FRASER CLARKE F/AU
E12         2   FRASER COLIN/AU
=> s e2-e4 and borrel?
L1         12 ("FRASER CLAIRE"/AU OR "FRASER CLAIRE M"/AU OR "FRASER CLAIRE
              MARIE"/AU) AND BORREL?
=> dup rem l1
PROCESSING COMPLETED FOR L1
L2          8 DUP REM L1 (4 DUPLICATES REMOVED)
=> d bib ab 1-
YOU HAVE REQUESTED DATA FROM 8 ANSWERS - CONTINUE? Y/(N):y
 L2  ANSWER 1 OF 8     MEDLINE on STN
AN  2004187163     MEDLINE
DN  PubMed ID: 15064399
TI  Comparison of the genome of the oral pathogen Treponema denticola with
    other spirochete genomes.
AU  Seshadri Rekha; Myers Garry S A; Tettelin Herve; Eisen Jonathan A;
    Heidelberg John F; Dodson Robert J; Davidsen Tanja M; DeBoy Robert T;
    Fouts Derrick E; Haft Dan H; Selengut Jeremy; Ren Qinghu; Brinkac Lauren
    M; Madupu Ramana; Kolonay Jamie; Durkin Scott A; Daugherty Sean C; Shetty
    Jyoti; Shvartsbeyn Alla; Gebregeorgis Elizabeth; Geer Keita; Tsegaye
    Getahun; Malek Joel; Ayodeji Bola; Shatsman Sofiya; McLeod Michael P;
    Smajs David; Howell Jerrilyn K; Pal Sangita; Amin Anita; Vashisth Pankaj;
    McNeill Thomas Z; Xiang Qin; Sodergren Erica; Baca Ernesto; Weinstock
    George M; Norris Steven J;  ***Fraser Claire M***  ; Paulsen Ian T
CS  The Institute for Genomic Research, 9712 Medical Center Drive, Rockville,
    MD 20850, USA.
NC  R01-DE12488 (NIDCR)
SO  Proceedings of the National Academy of Sciences of the United States of
    America, (2004 Apr 13) 101 (15) 5646-51.
    Journal code: 7505876. ISSN: 0027-8424.
CY  United States
DT  Journal; Article; (JOURNAL ARTICLE)
LA  English
FS  Priority Journals
OS  GENBANK-AE017226
EM  200405
ED  Entered STN: 20040415
    Last Updated on STN: 20040520
    Entered Medline: 20040519
AB  We present the complete 2,843,201-bp genome sequence of Treponema
    denticola (ATCC 35405) an oral spirochete associated with periodontal
    disease. Analysis of the T. denticola genome reveals factors mediating
    coaggregation, cell signaling, stress protection, and other competitive
    and cooperative measures, consistent with its pathogenic nature and
    lifestyle within the mixed-species environment of subgingival dental
    plaque. Comparisons with previously sequenced spirochete genomes revealed
    specific factors contributing to differences and similarities in
    spirochete physiology as well as pathogenic potential. The T. denticola
    genome is considerably larger in size than the genome of the related
    syphilis-causing spirochete Treponema pallidum. The differences in gene
    content appear to be attributable to a combination of three phenomena:
    genome reduction, lineage-specific expansions, and horizontal gene
    transfer. Genes lost due to reductive evolution appear to be largely
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involved in metabolism and transport, whereas some of the genes that have arisen due to lineage-specific expansions are implicated in various pathogenic interactions, and genes acquired via horizontal gene transfer are largely phage-related or of unknown function.

L2 ANSWER 2 OF 8 USPATFULL on STN
AN 2003:244254 USPATFULL
TI Nucleotide sequence of the Mycoplasma genitalium genome, fragments thereof, and uses thereof
IN ***Fraser, Claire M.*** , Potomac, MD, UNITED STATES
Adams, Mark D., Rockville, MD, UNITED STATES
Gocayne, Jeannine D., Potomac, MD, UNITED STATES
Hutchison, Clyde A., III, Chapel Hill, MD, UNITED STATES
Smith, Hamilton O., Reisterstown, MD, UNITED STATES
Venter, J. Craig, Queenstown, MD, UNITED STATES
White, Owen R., Rockville, MD, UNITED STATES
PA Johns Hopkins University, Baltimore, MD (U.S. corporation)
PI US 2003170663 A1 20030911
AI US 2002-205220 A1 20020726 (10)
RLI Division of Ser. No. US 1995-545528, filed on 19 Oct 1995, PENDING Continuation-in-part of Ser. No. US 1995-488018, filed on 7 Jun 1995, PENDING Continuation-in-part of Ser. No. US 1995-473545, filed on 7 Jun 1995, ABANDONED
DT Utility
FS APPLICATION
LREP HUMAN GENOME SCIENCES INC, 9410 KEY WEST AVENUE, ROCKVILLE, MD, 20850
CLMN Number of Claims: 19
ECL Exemplary Claim: 1
DRWN 23 Drawing Page(s)
LN.CNT 6270
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention provides the nucleotide sequence of the entire genome of Mycoplasma genitalium, SEQ ID NO: 1. The present invention further provides the sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use. In addition to the entire genomic sequence, the present invention identifies protein encoding fragments of the genome, and identifies, by position relative to two (2) genes known to flank the origin of replication, any regulatory elements which modulate the expression of the protein encoding fragments of the Mycoplasma genitalium genome.

L2 ANSWER 3 OF 8 USPATFULL on STN
AN 2003:81597 USPATFULL
TI Nucleotide sequence of the mycoplasma genitalium genome, fragments thereof, and uses thereof
IN ***Fraser, Claire M.*** , Potomac, MD, United States
Adams, Mark D., N. Potomac, MD, United States
Gocayne, Jeannine D., Silver Spring, MD, United States
Hutchison, III, Clyde A., Chapel Hill, NC, United States
Smith, Hamilton O., Towson, MD, United States
Venter, J. Craig, Potomac, MD, United States
White, Owen, Gaithersburg, MD, United States
PA The Institute for Genomic Research, Rockville, MD, United States (U.S. corporation)
Johns Hopkins University, Baltimore, MD, United States (U.S. corporation)
The University of North Carolina at Chapel Hill, Chapel Hill, NC, United States (U.S. corporation)
PI US 6537773 B1 20030325
AI US 1995-545528 19951019 (8)
RLI Continuation-in-part of Ser. No. US 1995-488018, filed on 7 Jun 1995, now abandoned Continuation-in-part of Ser. No. US 1995-473545, filed on 7 Jun 1995, now abandoned
DT Utility
FS GRANTED
EXNAM Primary Examiner: Ketter, James; Assistant Examiner: Schnizer, Richard
LREP Human Genome Sciences, Inc.

CLMN Number of Claims: 44
ECL Exemplary Claim: 1
DRWN 23 Drawing Figure(s); 23 Drawing Page(s)
LN.CNT 15190
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention provides the nucleotide sequence of the entire genome of Mycoplasma genitalium, SEQ ID NO:1. The present invention further provides the sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use. In addition to the entire genomic sequence, the present invention identifies protein encoding fragments of the genome, and identifies, by position relative to two (2) genes known to flank the origin of replication, any regulatory elements which modulate the expression of the protein encoding fragments of the Mycoplasma genitalium genome.

L2 ANSWER 4 OF 8 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 1
AN 2000:254050 BIOSIS
DN PREV200000254050
TI Distribution of twelve linear extrachromosomal DNAs in natural isolates of lyme disease spirochetes.
AU Palmer, Nanette; ***Fraser, Claire*** ; Casjens, Sherwood [Reprint author]
CS Department of Oncological Sciences, University of Utah Medical School, Salt Lake City, UT, 84132, USA
SO Journal of Bacteriology, (May, 2000) Vol. 182, No. 9, pp. 2476-2480. print.
CODEN: JOBAAY. ISSN: 0021-9193.
DT Article
LA English
ED Entered STN: 21 Jun 2000
Last Updated on STN: 5 Jan 2002
AB We have analyzed a panel of independent North American isolates of the Lyme disease agent spirochete, ***Borrelia*** burgdorferi (sensu stricto), for the presence of linear plasmids with sequence similarities to the 12 linear plasmids present in the B. burgdorferi type strain, isolate B31. The frequency of similarities to probes from each of the 12 B31 plasmids varied from 13 to 100% in the strain panel examined, and these similarities usually reside on plasmids similar in size to the cognate B31 plasmid. Sequences similar to 5 of the 12 B31 plasmids were found in all of the isolates examined, and >66% of the panel members hybridized to probes from 4 other plasmids. Sequences similar to most of the B. burgdorferi B31 plasmid-derived DNA probes used were also found on linear plasmids in the related Eurasian Lyme agents ***Borrelia*** garinii and ***Borrelia*** afzelii; however, some of these plasmids had uniform but substantially different sizes from their B. burgdorferi counterparts.

L2 ANSWER 5 OF 8 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 2
AN 2000:123164 BIOSIS
DN PREV200000123164
TI A bacterial genome in flux: The twelve linear and nine circular extrachromosomal DNAs in an infectious isolate of the Lyme disease spirochete ***Borrelia*** burgdorferi.
AU Casjens, Sherwood [Reprint author]; Palmer, Nanette; van Vugt, Rene; Huang, Wai Mun; Stevenson, Brian; Rosa, Patricia; Lathigra, Raju; Sutton, Granger; Peterson, Jeremy; Dodson, Robert J.; Haft, Daniel; Hickey, Erin; Gwinn, Michelle; White, Owen; ***Fraser, Claire M.***
CS Division of Molecular Biology and Genetics, Department of Oncological Sciences, University of Utah Medical School, Salt Lake City, UT, 84132, USA
SO Molecular Microbiology, (Feb., 2000) Vol. 35, No. 3, pp. 490-516. print.
CODEN: MOMIEE. ISSN: 0950-382X.
DT Article
LA English
ED Entered STN: 5 Apr 2000

Last Updated on STN: 3 Jan 2002

AB We have determined that ***Borrelia*** burgdorferi strain B31 MI carries 21 extrachromosomal DNA elements, the largest number known for any bacterium. Among these are 12 linear and nine circular plasmids, whose sequences total 610 694 bp. We report here the nucleotide sequence of three linear and seven circular plasmids (comprising 290 546 bp) in this infectious isolate. This completes the genome sequencing project for this organism; its genome size is 1 521 419 bp (plus about 2000 bp of undetermined telomeric sequences). Analysis of the sequence implies that there has been extensive and sometimes rather recent DNA rearrangement among a number of the linear plasmids. Many of these events appear to have been mediated by recombinational processes that formed duplications. These many regions of similarity are reflected in the fact that most plasmid genes are members of one of the genome's 161 paralogous gene families; 107 of these gene families, which vary in size from two to 41 members, contain at least one plasmid gene. These rearrangements appear to have contributed to a surprisingly large number of apparently non-functional pseudogenes, a very unusual feature for a prokaryotic genome. The presence of these damaged genes suggests that some of the plasmids may be in a period of rapid evolution. The sequence predicts 535 plasmid genes gtoreq300 bp in length that may be intact and 167 apparently mutationally damaged and/or unexpressed genes (pseudogenes). The large majority, over 90%, of genes on these plasmids have no convincing similarity to genes outside ***Borrelia*** , suggesting that they perform specialized functions.

L2 ANSWER 6 OF 8 CAPLUS COPYRIGHT 2004 ACS on STN

AN 1999:27841 CAPLUS

DN 130:62074

TI Nucleotide sequence of ***Borrelia*** burgdorferi genome and genomic fragments and open reading frames

IN ***Fraser, Claire*** ; White, Owen R.; Clayton, Rebecca; Dougherty, Brian A.; Lathigra, Raju; Smith, Hamilton O.

PA Human Genome Sciences, Inc., USA; Medimmune, Inc.

SO PCT Int. Appl., 1128 pp.
CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 2

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9858943	A1	19981230	WO 1998-US12764	19980618
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
CA 2304925	AA	19981230	CA 1998-2304925	19980618
AU 9881534	A1	19990104	AU 1998-81534	19980618
EP 1012157	A1	20000628	EP 1998-931389	19980618
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
PRAI US 1997-50359P	P	19970620		
US 1997-53344P	P	19970722		
US 1997-53377P	P	19970722		
US 1997-57483P	P	19970903		
WO 1998-US12764	W	19980618		

AB The present invention provides the complete nucleotide sequence of the ***Borrelia*** burgdorferi chromosome and 154 contigs representing the majority of the sequence of the B. burgdorferi extrachromosomal elements. Also provided are polypeptide sequences encoded by the polynucleotide sequences, corresponding polynucleotides and polypeptides, vectors and hosts comprising the polynucleotides, and assays and other uses thereof. Each open reading frame is identified with a function by homol. to a known

gene or polypeptide. The present invention further demonstrates that a large sequence can be sequenced using a random approach, eliminating the up front cost of isolating and ordering overlapping or contiguous subclones prior to the start of the sequencing protocols. The present invention further provides polynucleotide and polypeptide sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use.

RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 7 OF 8 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 3

AN 1998:361763 BIOSIS

DN PREV199800361763

TI Complete genome sequence of Treponema pallidum, the syphilis spirochete.

AU ***Fraser, Claire M.*** [Reprint author]; Norris, Steven J.; Weinstock, George M.; White, Owen; Sutton, Granger G.; Dodson, Robert; Gwinn, Michelle; Hickey, Erin K.; Clayton, Rebecca; Ketchum, Karen A.; Sodergren, Erica; Hardham, John M.; McLeod, Michael P.; Salzberg, Steven; Peterson, Jeremy; Khalak, Hanif; Richardson, Delwood; Howell, Jerrilyn K.; Chidambaram, Monjula; Utterback, Teresa; McDonald, Lisa; Artiach, Patricia; Bowman, Cheryl; Cotton, Matthew D.; Fujii, Claire; Garland, Stacey; Hatch, Bonnie; Horst, Kurt; Roberts, Kevin; Sandusky, Mina; Weidman, Janice; Smith, Hamilton O.; Venter, J. Craig

CS Inst. Genomic Res., 9712 Medical Center Drive, Rockville, MD 20850, USA

SO Science (Washington D C), (July 17, 1998) Vol. 281, No. 5375, pp. 375-388. print.
CODEN: SCIEAS. ISSN: 0036-8075.

DT Article

LA English

ED Entered STN: 27 Aug 1998
Last Updated on STN: 27 Aug 1998

AB The complete genome sequence of Treponema pallidum was determined and shown to be 1,138,006 base pairs containing 1041 predicted coding sequences (open reading frames). Systems for DNA replication, transcription, translation, and repair are intact, but catabolic and biosynthetic activities are minimized. The number of identifiable transporters is small, and no phosphoenolpyruvate: phosphotransferase carbohydrate transporters were found. Potential virulence factors include a family of 12 potential membrane proteins and several putative hemolysins. Comparison of the T. pallidum genome sequence with that of another pathogenic spirochete, ***Borrelia*** burgdorferi, the agent of Lyme disease, identified unique and common genes and substantiates the considerable diversity observed among pathogenic spirochetes.

L2 ANSWER 8 OF 8 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 4

AN 1998:46985 BIOSIS

DN PREV199800046985

TI Genomic sequence of a Lyme disease spirochaete, ***Borrelia*** burgdorferi.

AU ***Fraser, Claire M.*** [Reprint author]; Casjens, Sherwood; Huang, Wai Mun; Sutton, Granger G.; Clayton, Rebecca; Lathigra, Raju; White, Owen; Ketchum, Karen A.; Dodson, Robert; Hickey, Erin K.; Gwinn, Michelle; Dougherty, Brian; Tomb, Jean-Francois; Fleischmann, Robert D.; Richardson, Delwood; Peterson, Jeremy; Kerlavage, Anthony R.; Quackenbush, John; Salzberg, Steven; Hanson, Mark; Van Vugt, Rene; Palmer, Nanette; Adams, Mark D.; Gocayne, Jeannine; Weidman, Janice; Utterback, Teresa; Watthey, Larry; McDonald, Lisa; Artiach, Patricia; Bowman, Cheryl; Garland, Stacey; Fujii, Claire; Cotton, Matthew D.; Horst, Kurt; Roberts, Kevin; Hatch, Bonnie; Smith, Hamilton O.; Venter, J. Craig

CS Inst. Genomic Res., 9712 Medical Center Drive, Rockville, MD 20850, USA

SO Nature (London), (Dec. 11, 1997) Vol. 390, No. 6660, pp. 580-586. print.
CODEN: NATUAS. ISSN: 0028-0836.

DT Article

LA English

ED Entered STN: 27 Jan 1998

Last Updated on STN: 27 Jan 1998
AB The genome of the bacterium ***Borrelia*** burgdorferi B31, the aetiologic agent of Lyme disease, contains a linear chromosome of 910,725 base pairs and at least 17 linear and circular plasmids with a combined size of more than 533,000 base pairs. The chromosome contains 853 genes encoding a basic set of proteins for DNA replication, transcription, translation, solute transport and energy metabolism, but, like Mycoplasma genitalium, it contains no genes for cellular biosynthetic reactions. Because B. burgdorferi and M. genitalium are distantly related eubacteria, we suggest that their limited metabolic capacities reflect convergent evolution by gene loss from more metabolically competent progenitors. Of 430 genes on 11 plasmids, most have no known biological function; 39% of plasmid genes are paralogues that form 47 gene families. The biological significance of the multiple plasmid-encoded genes is not clear, although they may be involved in antigenic variation or immune evasion.

=> e white owen r/au
E1 1 WHITE OWEN L/AU
E2 1 WHITE OWEN LISTER/AU
E3 20 --> WHITE OWEN R/AU
E4 3 WHITE OWEN RICHARDSON/AU
E5 1524 WHITE P/AU
E6 432 WHITE P A/AU
E7 1 WHITE P A B/AU
E8 30 WHITE P A E/AU
E9 16 WHITE P A F/AU
E10 1 WHITE P A S/AU
E11 41 WHITE P B/AU
E12 1 WHITE P B D/AU

=> s e3-e4 and borrel?
L3 3 ("WHITE OWEN R"/AU OR "WHITE OWEN RICHARDSON"/AU) AND BORREL?

=> dup rem l3
PROCESSING COMPLETED FOR L3
L4 3 DUP REM L3 (0 DUPLICATES REMOVED)

=> d bib ab 1-
YOU HAVE REQUESTED DATA FROM 3 ANSWERS - CONTINUE? Y/(N):y

L4 ANSWER 1 OF 3 USPATFULL on STN
AN 2003:244254 USPATFULL
TI Nucleotide sequence of the Mycoplasma genitalium genome, fragments thereof, and uses thereof
IN Fraser, Claire M., Potomac, MD, UNITED STATES
Adams, Mark D., Rockville, MD, UNITED STATES
Gocayne, Jeannine D., Potomac, MD, UNITED STATES
Hutchison, Clyde A., III, Chapel Hill, MD, UNITED STATES
Smith, Hamilton O., Reisterstown, MD, UNITED STATES
Venter, J. Craig, Queenstown, MD, UNITED STATES
White, Owen R. , Rockville, MD, UNITED STATES
PA Johns Hopkins University, Baltimore, MD (U.S. corporation)
PI US 2003170663 A1 20030911
AI US 2002-205220 A1 20020726 (10)
RLI Division of Ser. No. US 1995-545528, filed on 19 Oct 1995, PENDING Continuation-in-part of Ser. No. US 1995-488018, filed on 7 Jun 1995, PENDING Continuation-in-part of Ser. No. US 1995-473545, filed on 7 Jun 1995, ABANDONED
DT Utility
FS APPLICATION
LREP HUMAN GENOME SCIENCES INC, 9410 KEY WEST AVENUE, ROCKVILLE, MD, 20850
CLMN Number of Claims: 19
ECL Exemplary Claim: 1
DRWN 23 Drawing Page(s)
LN.CNT 6270
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The present invention provides the nucleotide sequence of the entire genome of Mycoplasma genitalium, SEQ ID NO: 1. The present invention further provides the sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use. In addition to the entire genomic sequence, the present invention identifies protein encoding fragments of the genome, and identifies, by position relative to two (2) genes known to flank the origin of replication, any regulatory elements which modulate the expression of the protein encoding fragments of the Mycoplasma genitalium genome.

L4 ANSWER 2 OF 3 USPATFULL on STN
AN 2003:6806 USPATFULL
TI Selected polynucleotide and polypeptide sequences of the methanogenic archaeon, methanococcus jannashii
IN Bult, Carol J., Bar Harbor, ME, United States
White, Owen R. , Gaithersburg, MD, United States
Smith, Hamilton O., Baltimore, MD, United States
Woese, Carl R., Urbana, IL, United States
Venter, J. Craig, Rockville, MD, United States
PA The Board of Trustees of the University of Illinois, Urbana, IL, United States (U.S. corporation)
The Institute for Genomic Research, Rockville, MD, United States (U.S. corporation)
Johns Hopkins University, Baltimore, MD, United States (U.S. corporation)
PI US 6503729 B1 20030107
AI US 1997-916421 19970822 (8)
PRAI US 1996-24428P 19960822 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Ketter, James; Assistant Examiner: Schnizer, Richard
LREP Human Genome Sciences, Inc.
CLMN Number of Claims: 107
ECL Exemplary Claim: 1
DRWN 2 Drawing Figure(s); 2 Drawing Page(s)
LN.CNT 4244
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present application describes selected polynucleotide sequence from the 1.66-megabase pair genome sequence of an autotrophic archaeon, Methanococcus jannaschii, and its 58- and 16-kilobase pair extrachromosomal elements.

L4 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1999:27841 CAPLUS
DN 130:62074
TI Nucleotide sequence of ***Borrelia*** burgdorferi genome and genomic fragments and open reading frames
IN Fraser, Claire; ***White, Owen R.*** ; Clayton, Rebecca; Dougherty, Brian A.; Lathigra, Raju; Smith, Hamilton O.
PA Human Genome Sciences, Inc., USA; Medimmune, Inc.
SO PCT Int. Appl., 1128 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 2

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9858943	A1	19981230	WO 1998-US12764	19980618
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
CA 2304925	AA	19981230	CA 1998-2304925	19980618

AU 9881534 A1 19990104 AU 1998-81534 19980618
EP 1012157 A1 20000628 EP 1998-931389 19980618
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI
PRAI US 1997-50359P P 19970620
US 1997-53344P P 19970722
US 1997-53377P P 19970722
US 1997-57483P P 19970903
WO 1998-US12764 W 19980618
AB The present invention provides the complete nucleotide sequence of the ***Borrelia*** burgdorferi chromosome and 154 contigs representing the majority of the sequence of the B. burgdorferi extrachromosomal elements. Also provided are polypeptide sequences encoded by the polynucleotide sequences, corresponding polynucleotides and polypeptides, vectors and hosts comprising the polynucleotides, and assays and other uses thereof. Each open reading frame is identified with a function by homol. to a known gene or polypeptide. The present invention further demonstrates that a large sequence can be sequenced using a random approach, eliminating the up front cost of isolating and ordering overlapping or contiguous subclones prior to the start of the sequencing protocols. The present invention further provides polynucleotide and polypeptide sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use.
RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> e clayton rebecca/au
E1 19 CLAYTON RAYMOND B/AU
E2 1 CLAYTON REBECA/AU
E3 13 --> CLAYTON REBECCA/AU
E4 23 CLAYTON REBECCA A/AU
E5 2 CLAYTON REG F/AU
E6 1 CLAYTON REGINAL F/AU
E7 14 CLAYTON REGINALD F/AU
E8 1 CLAYTON REX/AU
E9 27 CLAYTON RICHARD/AU
E10 10 CLAYTON RICHARD A/AU
E11 1 CLAYTON RICHARD ANTHONY/AU
E12 3 CLAYTON RICHARD B/AU

=> s e2-e4 and borrel?
L5 5 ("CLAYTON REBECA"/AU OR "CLAYTON REBECCA"/AU OR "CLAYTON REBECCA A"/AU) AND BORREL?

=> dup rem l5
PROCESSING COMPLETED FOR L5
L6 3 DUP REM L5 (2 DUPLICATES REMOVED)

=> d bib ab 1-
YOU HAVE REQUESTED DATA FROM 3 ANSWERS - CONTINUE? Y/(N):y

L6 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1999:27841 CAPLUS
DN 130:62074
TI Nucleotide sequence of ***Borrelia*** burgdorferi genome and genomic fragments and open reading frames
IN Fraser, Claire; White, Owen R.; ***Clayton, Rebecca*** ; Dougherty, Brian A.; Lathigra, Raju; Smith, Hamilton O.
PA Human Genome Sciences, Inc., USA; Medimmune, Inc.
SO PCT Int. Appl., 1128 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 2
PATENT NO. KIND DATE APPLICATION NO. DATE
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PI WO 9858943 A1 19981230 WO 1998-US12764 19980618
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG
CA 2304925 AA 19981230 CA 1998-2304925 19980618
AU 9881534 A1 19990104 AU 1998-81534 19980618
EP 1012157 A1 20000628 EP 1998-931389 19980618
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI
PRAI US 1997-50359P P 19970620
US 1997-53344P P 19970722
US 1997-53377P P 19970722
US 1997-57483P P 19970903
WO 1998-US12764 W 19980618
AB The present invention provides the complete nucleotide sequence of the ***Borrelia*** burgdorferi chromosome and 154 contigs representing the majority of the sequence of the B. burgdorferi extrachromosomal elements. Also provided are polypeptide sequences encoded by the polynucleotide sequences, corresponding polynucleotides and polypeptides, vectors and hosts comprising the polynucleotides, and assays and other uses thereof. Each open reading frame is identified with a function by homol. to a known gene or polypeptide. The present invention further demonstrates that a large sequence can be sequenced using a random approach, eliminating the up front cost of isolating and ordering overlapping or contiguous subclones prior to the start of the sequencing protocols. The present invention further provides polynucleotide and polypeptide sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use.
RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 2 OF 3 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 1
AN 1998:361763 BIOSIS
DN PREV199800361763
TI Complete genome sequence of Treponema pallidum, the syphilis spirochete.
AU Fraser, Claire M. [Reprint author]; Norris, Steven J.; Weinstock, George M.; White, Owen; Sutton, Granger G.; Dodson, Robert; Gwinn, Michelle; Hickey, Erin K.; ***Clayton, Rebecca*** ; Ketchum, Karen A.; Sodergren, Erica; Hardham, John M.; McLeod, Michael P.; Salzberg, Steven; Peterson, Jeremy; Khalak, Hanif; Richardson, Delwood; Howell, Jerrilyn K.; Chidambaram, Monjula; Utterback, Teresa; McDonald, Lisa; Artiach, Patricia; Bowman, Cheryl; Cotton, Matthew D.; Fujii, Claire; Garland, Stacey; Hatch, Bonnie; Horst, Kurt; Roberts, Kevin; Sandusky, Mina; Weidman, Janice; Smith, Hamilton O.; Venter, J. Craig
CS Inst. Genomic Res., 9712 Medical Center Drive, Rockville, MD 20850, USA
SO Science (Washington D C), (July 17, 1998) Vol. 281, No. 5375, pp. 375-388. print.
CODEN: SCIEAS. ISSN: 0036-8075.
DT Article
LA English
ED Entered STN: 27 Aug 1998
Last Updated on STN: 27 Aug 1998
AB The complete genome sequence of Treponema pallidum was determined and shown to be 1,138,006 base pairs containing 1041 predicted coding sequences (open reading frames). Systems for DNA replication, transcription, translation, and repair are intact, but catabolic and biosynthetic activities are minimized. The number of identifiable transporters is small, and no phosphoenolpyruvate: phosphotransferase carbohydrate transporters were found. Potential virulence factors include a family of 12 potential membrane proteins and several putative hemolysins. Comparison of the T. pallidum genome sequence with that of

another pathogenic spirochete, ***Borrelia*** burgdorferi, the agent of Lyme disease, identified unique and common genes and substantiates the considerable diversity observed among pathogenic spirochetes.

L6 ANSWER 3 OF 3 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 2
AN 1998:46985 BIOSIS
DN PREV199800046985
TI Genomic sequence of a Lyme disease spirochaete, ***Borrelia*** burgdorferi.
AU Fraser, Claire M. [Reprint author]; Casjens, Sherwood; Huang, Wai Mun; Sutton, Granger G.; ***Clayton, Rebecca*** ; Lathigra, Raju; White, Owen; Ketchum, Karen A.; Dodson, Robert; Hickey, Erin K.; Gwinn, Michelle; Dougherty, Brian; Tomb, Jean-Francois; Fleischmann, Robert D.; Richardson, Delwood; Peterson, Jeremy; Kerlavage, Anthony R.; Quackenbush, John; Salzberg, Steven; Hanson, Mark; Van Vugt, Rene; Palmer, Nanette; Adams, Mark D.; Gocayne, Jeannine; Weidman, Janice; Utterback, Teresa; Watthey, Larry; McDonald, Lisa; Artiach, Patricia; Bowman, Cheryl; Garland, Stacey; Fujii, Claire; Cotton, Matthew D.; Horst, Kurt; Roberts, Kevin; Hatch, Bonnie; Smith, Hamilton O.; Venter, J. Craig
CS Inst. Genomic Res., 9712 Medical Center Drive, Rockville, MD 20850, USA
SO Nature (London), (Dec. 11, 1997) Vol. 390, No. 6660, pp. 580-586. print.
CODEN: NATUAS. ISSN: 0028-0836.
DT Article
LA English
ED Entered STN: 27 Jan 1998
Last Updated on STN: 27 Jan 1998
AB The genome of the bacterium ***Borrelia*** burgdorferi B31, the aetiologic agent of Lyme disease, contains a linear chromosome of 910,725 base pairs and at least 17 linear and circular plasmids with a combined size of more than 533,000 base pairs. The chromosome contains 853 genes encoding a basic set of proteins for DNA replication, transcription, translation, solute transport and energy metabolism, but, like Mycoplasma genitalium, it contains no genes for cellular biosynthetic reactions. Because B. burgdorferi and M. genitalium are distantly related eubacteria, we suggest that their limited metabolic capacities reflect convergent evolution by gene loss from more metabolically competent progenitors. Of 430 genes on 11 plasmids, most have no known biological function; 39% of plasmid genes are paralogues that form 47 gene families. The biological significance of the multiple plasmid-encoded genes is not clear, although they may be involved in antigenic variation or immune evasion.

=> e dougherty brian a/au
E1 1 DOUGHERTY BARRY/AU
E2 11 DOUGHERTY BRIAN/AU
E3 47 --> DOUGHERTY BRIAN A/AU
E4 1 DOUGHERTY BRIAN ANDREW/AU
E5 1 DOUGHERTY BRIAN C/AU
E6 9 DOUGHERTY BRIAN J/AU
E7 8 DOUGHERTY BRIAN L/AU
E8 1 DOUGHERTY BRIAN LYNN/AU
E9 17 DOUGHERTY BRIAN P/AU
E10 2 DOUGHERTY BRYAN/AU
E11 1 DOUGHERTY BRYAN ALVIN/AU
E12 131 DOUGHERTY C/AU

=> s e2-e4 and borrel?
L7 8 ("DOUGHERTY BRIAN"/AU OR "DOUGHERTY BRIAN A"/AU OR "DOUGHERTY BRIAN ANDREW"/AU) AND BORREL?

=> dup rem l7
PROCESSING COMPLETED FOR L7
L8 7 DUP REM L7 (1 DUPLICATE REMOVED)

=> d bib ab 1-
YOU HAVE REQUESTED DATA FROM 7 ANSWERS - CONTINUE? Y/(N):y

L8 ANSWER 1 OF 7 USPATFULL on STN
AN 2004:38579 USPATFULL
TI Streptococcus pneumoniae polynucleotides and sequences
IN Kunsch, Charles A., Norcross, GA, UNITED STATES
Choi, Gil H., Rockville, MD, UNITED STATES
Dillon, Patrick J., Carlsbad, CA, UNITED STATES
Rosen, Craig A., Laytonsville, MD, UNITED STATES
Barash, Steven C., Rockville, MD, UNITED STATES
Fannon, Michael R., Silver Spring, MD, UNITED STATES
Dougherty, Brian A. , Killingworth, CT, UNITED STATES
PA Human Genome Sciences, Inc., Rockville, MD, UNITED STATES, 20850 (U.S. corporation)
PI US 2004029118 A1 20040212
AI US 2002-158844 A1 20020603 (10)
RLI Division of Ser. No. US 1997-961527, filed on 30 Oct 1997, GRANTED, Pat. No. US 6420135
PRAI US 1996-29960P 19961031 (60)
DT Utility
FS APPLICATION
LREP HUMAN GENOME SCIENCES INC, 9410 KEY WEST AVENUE, ROCKVILLE, MD, 20850
CLMN Number of Claims: 20
ECL Exemplary Claim: 1
DRWN 2 Drawing Page(s)
LN.CNT 9165
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention provides polynucleotide sequences of the genome of Streptococcus pneumoniae, polypeptide sequences encoded by the polynucleotide sequences, corresponding polynucleotides and polypeptides, vectors and hosts comprising the polynucleotides, and assays and other uses thereof. The present invention further provides polynucleotide and polypeptide sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use.

L8 ANSWER 2 OF 7 USPATFULL on STN
AN 2003:148885 USPATFULL
TI Streptococcus pneumoniae antigens and vaccines
IN Choi, Gil H., Rockville, MD, United States
Kunsch, Charles A., Norcross, GA, United States
Barash, Steven C., Rockville, MD, United States
Dillon, Patrick J., Carlsbad, CA, United States
Dougherty, Brian , Killingworth, CT, United States
Fannon, Michael R., Silver Spring, MD, United States
Rosen, Craig A., Laytonsville, MD, United States
PA Human Genome Sciences, Inc., Rockville, MD, United States (U.S. corporation)
PI US 6573082 B1 20030603
AI US 2000-536784 20000328 (9)
RLI Continuation of Ser. No. US 1997-961083, filed on 30 Oct 1997
PRAI US 1996-29960P 19961031 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Navarro, Mark
LREP Human Genome Sciences, Inc.
CLMN Number of Claims: 21
ECL Exemplary Claim: 1
DRWN 0 Drawing Figure(s); 0 Drawing Page(s)
LN.CNT 5072
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to novel vaccines for the prevention or attenuation of infection by Streptococcus pneumoniae. The invention further relates to isolated nucleic acid molecules encoding antigenic polypeptides of Streptococcus pneumoniae. Antigenic polypeptides are also provided, as are vectors, host cells and recombinant methods for producing the same. The invention additionally relates to diagnostic methods for detecting Streptococcus nucleic acids, polypeptides and

antibodies in a biological sample.

L8 ANSWER 3 OF 7 USPATFULL on STN
AN 2002:119562 USPATFULL
TI Streptococcus pneumoniae antigens and vaccines
IN Choi, Gil H., Rockville, MD, UNITED STATES
Kunsch, Charles A., Norcross, GA, UNITED STATES
Barash, Steven C., Rockville, MD, UNITED STATES
Dillon, Patrick J., Carlsbad, CA, UNITED STATES
Dougherty, Brian , Killingworth, CT, UNITED STATES
Fannon, Michael R., Silver Spring, MD, UNITED STATES
Rosen, Craig A., Laytonsville, MD, UNITED STATES
PI US 2002061545 A1 20020523
AI US 2001-765272 A1 20010122 (9)
RLI Continuation of Ser. No. US 1997-961083, filed on 30 Oct 1997, UNKNOWN
DT Utility
FS APPLICATION
LREP HUMAN GENOME SCIENCES INC, 9410 KEY WEST AVENUE, ROCKVILLE, MD, 20850
CLMN Number of Claims: 21
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 5297
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to novel vaccines for the prevention or attenuation of infection by Streptococcus pneumoniae. The invention further relates to isolated nucleic acid molecules encoding antigenic polypeptides of Streptococcus pneumoniae. Antigenic polypeptides are also provided, as are vectors, host cells and recombinant methods for producing the same. The invention additionally relates to diagnostic methods for detecting Streptococcus nucleic acids, polypeptides and antibodies in a biological sample.

L8 ANSWER 4 OF 7 USPATFULL on STN
AN 2002:55159 USPATFULL
TI STREPTOCOCCUS PNEUMONIAE POLYNUCLEOTIDES AND SEQUENCES
IN KUNSCH, CHARLES A., GAITHERSBURG, MD, UNITED STATES
CHOI, GIL H., ROCKVILLE, MD, UNITED STATES
DILLON, PATRICK J., CARLSBAD, CA, UNITED STATES
ROSEN, CRAIG A., LAYTONSVILLE, MD, UNITED STATES
BARASH, STEVEN C., ROCKVILLE, MD, UNITED STATES
FANNON, MICHAEL R., SILVER SPRING, MD, UNITED STATES
DOUGHERTY, BRIAN A. , MT. AIRY, MD, UNITED STATES
PI US 2002032323 A1 20020314
US 6420135 B2 20020716
AI US 1997-961527 A1 19971030 (8)
PRAI US 1996-29960P 19961031 (60)
DT Utility
FS APPLICATION
LREP HUMAN GENOME SCIENCES INC, 9410 KEY WEST AVENUE, ROCKVILLE, MD, 20850
CLMN Number of Claims: 20
ECL Exemplary Claim: 1
DRWN 2 Drawing Page(s)
LN.CNT 7752
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention provides polynucleotide sequences of the genome of Streptococcus pneumoniae, polypeptide sequences encoded by the polynucleotide sequences, corresponding polynucleotides and polypeptides, vectors and hosts comprising the polynucleotides, and assays and other uses thereof. The present invention further provides polynucleotide and polypeptide sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use.

L8 ANSWER 5 OF 7 USPATFULL on STN
AN 2000:167517 USPATFULL
TI Streptococcus pneumoniae antigens and vaccines
IN Choi, Gil H., Rockville, MD, United States

Kunsch, Charles A., Atlanta, GA, United States
Barash, Steven C., Rockville, MD, United States
Dillon, Patrick J., Carlsbad, CA, United States
Dougherty, Brian , Killingworth, CT, United States
Fannon, Michael R., Silver Spring, MD, United States
Rosen, Craig A., Laytonsville, MD, United States
PA Human Genome Sciences, Inc., Rockville, MD, United States (U.S. corporation)
PI US 6159469 20001212
AI US 1997-961083 19971030 (8)
PRAI US 1996-29960P 19961031 (60)
DT Utility
FS Granted
EXNAM Primary Examiner: Housel, James C.; Assistant Examiner: Hines, Ja-Na A.
LREP Human Genome Sciences, Inc.
CLMN Number of Claims: 73
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 13121
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to novel vaccines for the prevention or attenuation of infection by Streptococcus pneumoniae. The invention further relates to isolated nucleic acid molecules encoding antigenic polypeptides of Streptococcus pneumoniae. Antigenic polypeptides are also provided, as are vectors, host cells and recombinant methods for producing the same. The invention additionally relates to diagnostic methods for detecting Streptococcus nucleic acids, polypeptides and antibodies in a biological sample.

L8 ANSWER 6 OF 7 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1999:27841 CAPLUS
DN 130:62074
TI Nucleotide sequence of ***Borrelia*** burgdorferi genome and genomic fragments and open reading frames
IN Fraser, Claire; White, Owen R.; Clayton, Rebecca; ***Dougherty, Brian*** *** A.*** ; Lathigra, Raju; Smith, Hamilton O.
PA Human Genome Sciences, Inc., USA; Medimmune, Inc.
SO PCT Int. Appl., 1128 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 2

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9858943	A1	19981230	WO 1998-US12764	19980618
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
CA 2304925	AA	19981230	CA 1998-2304925	19980618
AU 9881534	A1	19990104	AU 1998-81534	19980618
EP 1012157	A1	20000628	EP 1998-931389	19980618
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				

PRAI US 1997-50359P P 19970620
US 1997-53344P P 19970722
US 1997-53377P P 19970722
US 1997-57483P P 19970903
WO 1998-US12764 W 19980618
AB The present invention provides the complete nucleotide sequence of the ***Borrelia*** burgdorferi chromosome and 154 contigs representing the majority of the sequence of the B. burgdorferi extrachromosomal elements. Also provided are polypeptide sequences encoded by the polynucleotide

sequences, corresponding polynucleotides and polypeptides, vectors and hosts comprising the polynucleotides, and assays and other uses thereof. Each open reading frame is identified with a function by homol. to a known gene or polypeptide. The present invention further demonstrates that a large sequence can be sequenced using a random approach, eliminating the up front cost of isolating and ordering overlapping or contiguous subclones prior to the start of the sequencing protocols. The present invention further provides polynucleotide and polypeptide sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use.

RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 7 OF 7 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 1
AN 1998:46985 BIOSIS
DN PREV199800046985
TI Genomic sequence of a Lyme disease spirochaete, ***Borrelia*** burgdorferi.
AU Fraser, Claire M. [Reprint author]; Casjens, Sherwood; Huang, Wai Mun; Sutton, Granger G.; Clayton, Rebecca; Lathigra, Raju; White, Owen; Ketchum, Karen A.; Dodson, Robert; Hickey, Erin K.; Gwinn, Michelle; ***Dougherty, Brian*** ; Tomb, Jean-Francois; Fleischmann, Robert D.; Richardson, Delwood; Peterson, Jeremy; Kerlavage, Anthony R.; Quackenbush, John; Salzberg, Steven; Hanson, Mark; Van Vugt, Rene; Palmer, Nanette; Adams, Mark D.; Gocayne, Jeannine; Weidman, Janice; Utterback, Teresa; Watthey, Larry; McDonald, Lisa; Artiach, Patricia; Bowman, Cheryl; Garland, Stacey; Fujii, Claire; Cotton, Matthew D.; Horst, Kurt; Roberts, Kevin; Hatch, Bonnie; Smith, Hamilton O.; Venter, J. Craig
CS Inst. Genomic Res., 9712 Medical Center Drive, Rockville, MD 20850, USA
SO Nature (London), (Dec. 11, 1997) Vol. 390, No. 6660, pp. 580-586. print. CODEN: NATUAS. ISSN: 0028-0836.
DT Article
LA English
ED Entered STN: 27 Jan 1998
Last Updated on STN: 27 Jan 1998
AB The genome of the bacterium ***Borrelia*** burgdorferi B31, the aetiologic agent of Lyme disease, contains a linear chromosome of 910,725 base pairs and at least 17 linear and circular plasmids with a combined size of more than 533,000 base pairs. The chromosome contains 853 genes encoding a basic set of proteins for DNA replication, transcription, translation, solute transport and energy metabolism, but, like Mycoplasma genitalium, it contains no genes for cellular biosynthetic reactions. Because B. burgdorferi and M. genitalium are distantly related eubacteria, we suggest that their limited metabolic capacities reflect convergent evolution by gene loss from more metabolically competent progenitors. Of 430 genes on 11 plasmids, most have no known biological function; 39% of plasmid genes are paralogues that form 47 gene families. The biological significance of the multiple plasmid-encoded genes is not clear, although they may be involved in antigenic variation or immune evasion.

=> e lathigra raju/au
E1 112 LATHIGRA R/AU
E2 15 LATHIGRA R B/AU
E3 29 --> LATHIGRA RAJU/AU
E4 2 LATHIGRA RAJU B/AU
E5 1 LATHIGRA RUJU/AU
E6 30 LATHIKA K M/AU
E7 2 LATHIKA KUNNATHATTU M/AU
E8 3 LATHIKA N/AU
E9 2 LATHIKA NAIR/AU
E10 4 LATHIKA P/AU
E11 4 LATHIM D/AU
E12 2 LATHIM DELBERT L/AU

=> s e1-e5 and borrel?

L9 24 ("LATHIGRA R"/AU OR "LATHIGRA R B"/AU OR "LATHIGRA RAJU"/AU OR "LATHIGRA RAJU B"/AU OR "LATHIGRA RUJU"/AU) AND BORREL?

=> dup rem l9
PROCESSING COMPLETED FOR L9
L10 6 DUP REM L9 (18 DUPLICATES REMOVED)

=> d bib ab 1-
YOU HAVE REQUESTED DATA FROM 6 ANSWERS - CONTINUE? Y/(N):y

L10 ANSWER 1 OF 6 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:260328 CAPLUS
DN 132:307239
TI Decorin binding proteins DBP A and B and genes encoding them
IN Hanson, Mark S.; Mullikin, Brian A.; Roberts, William; ***Lathigra,*** *** Raju***
PA Medimmune, Inc., USA
SO PCT Int. Appl., 93 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000021989	A1	20000420	WO 1999-US23481	19991008
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
EP 1135409	A1	20010926	EP 1999-954795	19991008
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
PRAI US 1998-103728P	P	19981009		
WO 1999-US23481	W	19991008		

AB The present invention provides bacterial immunogenic agents for administration to humans and non-human animals to stimulate an immune response. It particularly relates to the vaccination of mammalian species with polypeptides derived from bacterial species that cause Lyme disease as a mechanism for stimulating prodn. of antibodies that protect the vaccine recipient against infection by such pathogenic bacterial species, or make the recipient more resistant to such infection. In another aspect the invention provides antibodies against such proteins and protein complexes that may be used as diagnostics and/or as protective/treatment agents for pathogenic bacterial species.
RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L10 ANSWER 2 OF 6 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 1
AN 2000:123164 BIOSIS
DN PREV200000123164
TI A bacterial genome in flux: The twelve linear and nine circular extrachromosomal DNAs in an infectious isolate of the Lyme disease spirochete ***Borrelia*** burgdorferi.
AU Casjens, Sherwood [Reprint author]; Palmer, Nanette; van Vugt, Rene; Huang, Wai Mun; Stevenson, Brian; Rosa, Patricia; ***Lathigra, Raju*** ; Sutton, Granger; Peterson, Jeremy; Dodson, Robert J.; Haft, Daniel; Hickey, Erin; Gwinn, Michelle; White, Owen; Fraser, Claire M.
CS Division of Molecular Biology and Genetics, Department of Oncological Sciences, University of Utah Medical School, Salt Lake City, UT, 84132, USA
SO Molecular Microbiology, (Feb., 2000) Vol. 35, No. 3, pp. 490-516. print.

CODEN: MOMIEE. ISSN: 0950-382X.
DT Article
LA English
ED Entered STN: 5 Apr 2000
Last Updated on STN: 3 Jan 2002
AB We have determined that ***Borrelia*** burgdorferi strain B31 MI carries 21 extrachromosomal DNA elements, the largest number known for any bacterium. Among these are 12 linear and nine circular plasmids, whose sequences total 610 694 bp. We report here the nucleotide sequence of three linear and seven circular plasmids (comprising 290 546 bp) in this infectious isolate. This completes the genome sequencing project for this organism; its genome size is 1 521 419 bp (plus about 2000 bp of undetermined telomeric sequences). Analysis of the sequence implies that there has been extensive and sometimes rather recent DNA rearrangement among a number of the linear plasmids. Many of these events appear to have been mediated by recombinational processes that formed duplications. These many regions of similarity are reflected in the fact that most plasmid genes are members of one of the genome's 161 paralogous gene families; 107 of these gene families, which vary in size from two to 41 members, contain at least one plasmid gene. These rearrangements appear to have contributed to a surprisingly large number of apparently non-functional pseudogenes, a very unusual feature for a prokaryotic genome. The presence of these damaged genes suggests that some of the plasmids may be in a period of rapid evolution. The sequence predicts 535 plasmid genes gtoreq300 bp in length that may be intact and 167 apparently mutationally damaged and/or unexpressed genes (pseudogenes). The large majority, over 90%, of genes on these plasmids have no convincing similarity to genes outside ***Borrelia*** , suggesting that they perform specialized functions.

L10 ANSWER 3 OF 6 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1999:27959 CAPLUS
DN 130:109198
TI ***Borrelia*** polynucleotides and antigenic polypeptides for use as Lyme disease vaccines and diagnostics
IN Choi, Gil H.; Erwin, Alice L.; Hanson, Mark S.; ***Lathigra, Raju***
PA Human Genome Sciences, Inc., USA; Medimmune, Inc.
SO PCT Int. Appl., 275 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 2

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9859071	A1	19981230	WO 1998-US12718	19980618
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
AU 9881518	A1	19990104	AU 1998-81518	19980618
EP 1009859	A1	20000621	EP 1998-931370	19980618
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				

PRAI US 1997-50359P	P	19970620
US 1997-53344P	P	19970722
US 1997-53377P	P	19970722
US 1997-57483P	P	19970903
WO 1998-US12718	W	19980618

AB The present invention relates to novel vaccines for the prevention or attenuation of Lyme disease. The invention further relates to isolated nucleic acid mols. encoding antigenic polypeptides of ***Borrelia*** burgdorferi. Also provided are antigenic polypeptides for use as vaccine and antibodies for diagnosis, as are vectors, host cells and recombinant

methods for producing the same. The invention addnl. relates to diagnostic methods for detecting ***Borrelia*** gene expression.
RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L10 ANSWER 4 OF 6 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1999:27841 CAPLUS
DN 130:62074
TI Nucleotide sequence of ***Borrelia*** burgdorferi genome and genomic fragments and open reading frames
IN Fraser, Claire; White, Owen R.; Clayton, Rebecca; Dougherty, Brian A.; ***Lathigra, Raju*** ; Smith, Hamilton O.
PA Human Genome Sciences, Inc., USA; Medimmune, Inc.
SO PCT Int. Appl., 1128 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 2

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9858943	A1	19981230	WO 1998-US12764	19980618
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
CA 2304925	AA	19981230	CA 1998-2304925	19980618
AU 9881534	A1	19990104	AU 1998-81534	19980618
EP 1012157	A1	20000628	EP 1998-931389	19980618
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				

PRAI US 1997-50359P P 19970620
US 1997-53344P P 19970722
US 1997-53377P P 19970722
US 1997-57483P P 19970903
WO 1998-US12764 W 19980618
AB The present invention provides the complete nucleotide sequence of the ***Borrelia*** burgdorferi chromosome and 154 contigs representing the majority of the sequence of the B. burgdorferi extrachromosomal elements. Also provided are polypeptide sequences encoded by the polynucleotide sequences, corresponding polynucleotides and polypeptides, vectors and hosts comprising the polynucleotides, and assays and other uses thereof. Each open reading frame is identified with a function by homol. to a known gene or polypeptide. The present invention further demonstrates that a large sequence can be sequenced using a random approach, eliminating the up front cost of isolating and ordering overlapping or contiguous subclones prior to the start of the sequencing protocols. The present invention further provides polynucleotide and polypeptide sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use.
RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L10 ANSWER 5 OF 6 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 2
AN 1998:510282 BIOSIS
DN PREV199800510282
TI Molecular analysis of sequence heterogeneity among genes encoding decorin binding proteins A and B of ***Borrelia*** burgdorferi sensu lato.
AU Roberts, William C.; Mullikin, Brian A.; ***Lathigra, Raju*** ; Hanson, Mark S. [Reprint author]
CS MedImmune Inc., 35 West Watkins Mill Road, Gaithersburg, MD 20878, USA
SO Infection and Immunity, (Nov., 1998) Vol. 66, No. 11, pp. 5275-5285. print.

CODEN: INFIBR. ISSN: 0019-9567.
DT Article
LA English
ED Entered STN: 18 Dec 1998
Last Updated on STN: 18 Dec 1998
AB Immunization of mice with ***Borrelia*** burgdorferi decorin binding protein A (DbpA), one of two gene products of the dbpBA locus, has been shown recently to confer protection against challenge. Hyperimmune DbpA antiserum killed a large number of B. burgdorferi sensu lato isolates of diverse phylogeny and origin, suggesting conservation of the protective epitope(s). In order to evaluate the heterogeneity of DbpA and DbpB and to facilitate defining the conserved epitope(s) of these antigens, the sequences of the dbpA genes from 29 B. burgdorferi sensu lato isolates and of the dbpb genes from 15 B. burgdorferi sensu lato isolates were determined. The predicted DbpA sequences were fairly heterogeneous among the isolates (58.3 to 100% similarity), but DbpA sequences with the highest similarity tended to group into species previously defined by well-characterized chromosomal markers. In contrast, the predicted DbpB sequences were highly conserved (96.3 to 100% similarity). Substantial diversity in DbpA sequence was seen among isolates previously shown to be killed by antiserum against a single DbpA, suggesting that one or more conserved protective epitopes are composed of noncontiguous amino acids. The observation of individual dbpA alleles with sequence elements characteristic of more than one B. burgdorferi sensu lato species was consistent with a role for genetic recombination in the generation of dbpA diversity.

L10 ANSWER 6 OF 6 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 3
AN 1998:46985 BIOSIS
DN PREV199800046985
TI Genomic sequence of a Lyme disease spirochaete, ***Borrelia*** burgdorferi.
AU Fraser, Claire M. [Reprint author]; Casjens, Sherwood; Huang, Wai Mun; Sutton, Granger G.; Clayton, Rebecca; ***Lathigra, Raju*** ; White, Owen; Ketchum, Karen A.; Dodson, Robert; Hickey, Erin K.; Gwinn, Michelle; Dougherty, Brian; Tomb, Jean-Francois; Fleischmann, Robert D.; Richardson, Delwood; Peterson, Jeremy; Kerlavage, Anthony R.; Quackenbush, John; Salzberg, Steven; Hanson, Mark; Van Vugt, Rene; Palmer, Nanette; Adams, Mark D.; Gocayne, Jeannine; Weidman, Janice; Utterback, Teresa; Watthey, Larry; McDonald, Lisa; Artiach, Patricia; Bowman, Cheryl; Garland, Stacey; Fujii, Claire; Cotton, Matthew D.; Horst, Kurt; Roberts, Kevin; Hatch, Bonnie; Smith, Hamilton O.; Venter, J. Craig
CS Inst. Genomic Res., 9712 Medical Center Drive, Rockville, MD 20850, USA
SO Nature (London), (Dec. 11, 1997) Vol. 390, No. 6660, pp. 580-586. print.
CODEN: NATUAS. ISSN: 0028-0836.
DT Article
LA English
ED Entered STN: 27 Jan 1998
Last Updated on STN: 27 Jan 1998
AB The genome of the bacterium ***Borrelia*** burgdorferi B31, the aetiologic agent of Lyme disease, contains a linear chromosome of 910,725 base pairs and at least 17 linear and circular plasmids with a combined size of more than 533,000 base pairs. The chromosome contains 853 genes encoding a basic set of proteins for DNA replication, transcription, translation, solute transport and energy metabolism, but, like Mycoplasma genitalium, it contains no genes for cellular biosynthetic reactions. Because B. burgdorferi and M. genitalium are distantly related eubacteria, we suggest that their limited metabolic capacities reflect convergent evolution by gene loss from more metabolically competent progenitors. Of 430 genes on 11 plasmids, most have no known biological function; 39% of plasmid genes are paralogues that form 47 gene families. The biological significance of the multiple plasmid-encoded genes is not clear, although they may be involved in antigenic variation or immune evasion.

=> e smith hamilton o/au

E1 1 SMITH HALLAM C/AU
E2 56 SMITH HAMILTON/AU
E3 164 --> SMITH HAMILTON O/AU
E4 4 SMITH HAMILTON OTHANEL/AU
E5 39 SMITH HAMISH R C/AU
E6 3 SMITH HAMMOND C/AU
E7 7 SMITH HAMMOND C A/AU
E8 2 SMITH HAMMOND CAROL A/AU
E9 1 SMITH HAMPTON/AU
E10 2 SMITH HAMPTON D/AU
E11 11 SMITH HAMPTON D JR/AU
E12 1 SMITH HAMPTON DAVID JR/AU

=> s e2-e4 and borrel?
L11 8 ("SMITH HAMILTON"/AU OR "SMITH HAMILTON O"/AU OR "SMITH HAMILTON OTHANEL"/AU) AND BORREL?

=> dup rem l11
PROCESSING COMPLETED FOR L11
L12 6 DUP REM L11 (2 DUPLICATES REMOVED)

=> d bib ab 1-
YOU HAVE REQUESTED DATA FROM 6 ANSWERS - CONTINUE? Y/(N):y

L12 ANSWER 1 OF 6 USPATFULL on STN
AN 2003:244254 USPATFULL
TI Nucleotide sequence of the Mycoplasma genitalium genome, fragments thereof, and uses thereof
IN Fraser, Claire M., Potomac, MD, UNITED STATES
Adams, Mark D., Rockville, MD, UNITED STATES
Gocayne, Jeannine D., Potomac, MD, UNITED STATES
Hutchison, Clyde A., III, Chapel Hill, MD, UNITED STATES
Smith, Hamilton O. , Reisterstown, MD, UNITED STATES
Venter, J. Craig, Queenstown, MD, UNITED STATES
White, Owen R., Rockville, MD, UNITED STATES
PA Johns Hopkins University, Baltimore, MD (U.S. corporation)
PI US 2003170663 A1 20030911
AI US 2002-205220 A1 20020726 (10)
RLI Division of Ser. No. US 1995-545528, filed on 19 Oct 1995, PENDING Continuation-in-part of Ser. No. US 1995-488018, filed on 7 Jun 1995, PENDING Continuation-in-part of Ser. No. US 1995-473545, filed on 7 Jun 1995, ABANDONED
DT Utility
FS APPLICATION
LREP HUMAN GENOME SCIENCES INC, 9410 KEY WEST AVENUE, ROCKVILLE, MD, 20850
CLMN Number of Claims: 19
ECL Exemplary Claim: 1
DRWN 23 Drawing Page(s)
LN.CNT 6270
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention provides the nucleotide sequence of the entire genome of Mycoplasma genitalium, SEQ ID NO: 1. The present invention further provides the sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use. In addition to the entire genomic sequence, the present invention identifies protein encoding fragments of the genome, and identifies, by position relative to two (2) genes known to flank the origin of replication, any regulatory elements which modulate the expression of the protein encoding fragments of the Mycoplasma genitalium genome.

L12 ANSWER 2 OF 6 USPATFULL on STN
AN 2003:81597 USPATFULL
TI Nucleotide sequence of the mycoplasma genitalium genome, fragments thereof, and uses thereof
IN Fraser, Claire M., Potomac, MD, United States
Adams, Mark D., N. Potomac, MD, United States

Gocayne, Jeannine D., Silver Spring, MD, United States
Hutchison, III, Clyde A., Chapel Hill, NC, United States
Smith, Hamilton O. , Towson, MD, United States
Venter, J. Craig, Potomac, MD, United States
White, Owen, Gaithersburg, MD, United States
PA The Institute for Genomic Research, Rockville, MD, United States (U.S. corporation)
Johns Hopkins University, Baltimore, MD, United States (U.S. corporation)
The University of North Carolina at Chapel Hill, Chapel Hill, NC, United States (U.S. corporation)
PI US 6537773 B1 20030325
AI US 1995-545528 19951019 (8)
RLI Continuation-in-part of Ser. No. US 1995-488018, filed on 7 Jun 1995, now abandoned Continuation-in-part of Ser. No. US 1995-473545, filed on 7 Jun 1995, now abandoned
DT Utility
FS GRANTED
EXNAM Primary Examiner: Ketter, James; Assistant Examiner: Schnizer, Richard
LREP Human Genome Sciences, Inc.
CLMN Number of Claims: 44
ECL Exemplary Claim: 1
DRWN 23 Drawing Figure(s); 23 Drawing Page(s)
LN.CNT 15190
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention provides the nucleotide sequence of the entire genome of Mycoplasma genitalium, SEQ ID NO:1. The present invention further provides the sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use. In addition to the entire genomic sequence, the present invention identifies protein encoding fragments of the genome, and identifies, by position relative to two (2) genes known to flank the origin of replication, any regulatory elements which modulate the expression of the protein encoding fragments of the Mycoplasma genitalium genome.

L12 ANSWER 3 OF 6 USPATFULL on STN
AN 2003:6806 USPATFULL
TI Selected polynucleotide and polypeptide sequences of the methanogenic archaeon, methanococcus jannashii
IN Bult, Carol J., Bar Harbor, ME, United States
White, Owen R., Gaithersburg, MD, United States
Smith, Hamilton O. , Baltimore, MD, United States
Woese, Carl R., Urbana, IL, United States
Venter, J. Craig, Rockville, MD, United States
PA The Board of Trustees of the University of Illinois, Urbana, IL, United States (U.S. corporation)
The Institute for Genomic Research, Rockville, MD, United States (U.S. corporation)
Johns Hopkins University, Baltimore, MD, United States (U.S. corporation)
PI US 6503729 B1 20030107
AI US 1997-916421 19970822 (8)
PRAI US 1996-24428P 19960822 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Ketter, James; Assistant Examiner: Schnizer, Richard
LREP Human Genome Sciences, Inc.
CLMN Number of Claims: 107
ECL Exemplary Claim: 1
DRWN 2 Drawing Figure(s); 2 Drawing Page(s)
LN.CNT 4244
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present application describes selected polynucleotide sequence from the 1.66-megabase pair genome sequence of an autotrophic archaeon, Methanococcus jannaschii, and its 58- and 16-kilobase pair extrachromosomal elements.

L12 ANSWER 4 OF 6 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1999:27841 CAPLUS
DN 130:62074
TI Nucleotide sequence of ***Borrelia*** burgdorferi genome and genomic fragments and open reading frames
IN Fraser, Claire; White, Owen R.; Clayton, Rebecca; Dougherty, Brian A.; Lathigra, Raju; ***Smith, Hamilton O.***
PA Human Genome Sciences, Inc., USA; Medimmune, Inc.
SO PCT Int. Appl., 1128 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 2

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9858943	A1	19981230	WO 1998-US12764	19980618
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
CA 2304925	AA	19981230	CA 1998-2304925	19980618
AU 9881534	A1	19990104	AU 1998-81534	19980618
EP 1012157	A1	20000628	EP 1998-931389	19980618
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				

PRAI US 1997-50359P P 19970620
US 1997-53344P P 19970722
US 1997-53377P P 19970722
US 1997-57483P P 19970903
WO 1998-US12764 W 19980618
AB The present invention provides the complete nucleotide sequence of the ***Borrelia*** burgdorferi chromosome and 154 contigs representing the majority of the sequence of the B. burgdorferi extrachromosomal elements. Also provided are polypeptide sequences encoded by the polynucleotide sequences, corresponding polynucleotides and polypeptides, vectors and hosts comprising the polynucleotides, and assays and other uses thereof. Each open reading frame is identified with a function by homol. to a known gene or polypeptide. The present invention further demonstrates that a large sequence can be sequenced using a random approach, eliminating the up front cost of isolating and ordering overlapping or contiguous subclones prior to the start of the sequencing protocols. The present invention further provides polynucleotide and polypeptide sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use.
RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 5 OF 6 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 1
AN 1998:361763 BIOSIS
DN PREV199800361763
TI Complete genome sequence of Treponema pallidum, the syphilis spirochete.
AU Fraser, Claire M. [Reprint author]; Norris, Steven J.; Weinstock, George M.; White, Owen; Sutton, Granger G.; Dodson, Robert; Gwinn, Michelle; Hickey, Erin K.; Clayton, Rebecca; Ketchum, Karen A.; Sodergren, Erica; Hardham, John M.; McLeod, Michael P.; Salzberg, Steven; Peterson, Jeremy; Khalak, Hanif; Richardson, Delwood; Howell, Jerrilyn K.; Chidambaram, Monjula; Utterback, Teresa; McDonald, Lisa; Artiach, Patricia; Bowman, Cheryl; Cotton, Matthew D.; Fujii, Claire; Garland, Stacey; Hatch, Bonnie; Horst, Kurt; Roberts, Kevin; Sandusky, Mina; Weidman, Janice; ***Smith,*** *** Hamilton O.*** ; Venter, J. Craig
CS Inst. Genomic Res., 9712 Medical Center Drive, Rockville, MD 20850, USA
SO Science (Washington D C), (July 17, 1998) Vol. 281, No. 5375, pp. 375-388.

print.
CODEN: SCIEAS. ISSN: 0036-8075.
DT Article
LA English
ED Entered STN: 27 Aug 1998
Last Updated on STN: 27 Aug 1998
AB The complete genome sequence of Treponema pallidum was determined and shown to be 1,138,006 base pairs containing 1041 predicted coding sequences (open reading frames). Systems for DNA replication, transcription, translation, and repair are intact, but catabolic and biosynthetic activities are minimized. The number of identifiable transporters is small, and no phosphoenolpyruvate: phosphotransferase carbohydrate transporters were found. Potential virulence factors include a family of 12 potential membrane proteins and several putative hemolysins. Comparison of the T. pallidum genome sequence with that of another pathogenic spirochete, ***Borrelia*** burgdorferi, the agent of Lyme disease, identified unique and common genes and substantiates the considerable diversity observed among pathogenic spirochetes.

L12 ANSWER 6 OF 6 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 2
AN 1998:46985 BIOSIS
DN PREV199800046985
TI Genomic sequence of a Lyme disease spirochaete, ***Borrelia*** burgdorferi.
AU Fraser, Claire M. [Reprint author]; Casjens, Sherwood; Huang, Wai Mun; Sutton, Granger G.; Clayton, Rebecca; Lathigra, Raju; White, Owen; Ketchum, Karen A.; Dodson, Robert; Hickey, Erin K.; Gwinn, Michelle; Dougherty, Brian; Tomb, Jean-Francois; Fleischmann, Robert D.; Richardson, Delwood; Peterson, Jeremy; Kerlavage, Anthony R.; Quackenbush, John; Salzberg, Steven; Hanson, Mark; Van Vugt, Rene; Palmer, Nanette; Adams, Mark D.; Gocayne, Jeannine; Weidman, Janice; Utterback, Teresa; Watthey, Larry; McDonald, Lisa; Artiach, Patricia; Bowman, Cheryl; Garland, Stacey; Fujii, Claire; Cotton, Matthew D.; Horst, Kurt; Roberts, Kevin; Hatch, Bonnie; ***Smith, Hamilton O.*** ; Venter, J. Craig
CS Inst. Genomic Res., 9712 Medical Center Drive, Rockville, MD 20850, USA
SO Nature (London), (Dec. 11, 1997) Vol. 390, No. 6660, pp. 580-586. print.
CODEN: NATUAS. ISSN: 0028-0836.
DT Article
LA English
ED Entered STN: 27 Jan 1998
Last Updated on STN: 27 Jan 1998
AB The genome of the bacterium ***Borrelia*** burgdorferi B31, the aetiologic agent of Lyme disease, contains a linear chromosome of 910,725 base pairs and at least 17 linear and circular plasmids with a combined size of more than 533,000 base pairs. The chromosome contains 853 genes encoding a basic set of proteins for DNA replication, transcription, translation, solute transport and energy metabolism, but, like Mycoplasma genitalium, it contains no genes for cellular biosynthetic reactions. Because B. burgdorferi and M. genitalium are distantly related eubacteria, we suggest that their limited metabolic capacities reflect convergent evolution by gene loss from more metabolically competent progenitors. Of 430 genes on 11 plasmids, most have no known biological function; 39% of plasmid genes are paralogues that form 47 gene families. The biological significance of the multiple plasmid-encoded genes is not clear, although they may be involved in antigenic variation or immune evasion.

=> e casjens sherwood/au
E1 53 CASJENS S R/AU
E2 1 CASJENS SH/AU
E3 116 --> CASJENS SHERWOOD/AU
E4 19 CASJENS SHERWOOD R/AU
E5 1 CASJENS SHERWOOD REID/AU
E6 4 CASJKA C/AU
E7 3 CASJKA CHANTAL/AU
E8 2 CASKA B/AU

E9 2 CASKA B A/AU
E10 2 CASKA BARBARA/AU
E11 3 CASKA JOSEF/AU
E12 4 CASKADON M A/AU

=> s e1-e5 and borrel?
L13 46 ("CASJENS S R"/AU OR "CASJENS SH"/AU OR "CASJENS SHERWOOD"/AU OR "CASJENS SHERWOOD R"/AU OR "CASJENS SHERWOOD REID"/AU) AND BORREL?

=> dup rem l13
PROCESSING COMPLETED FOR L13
L14 26 DUP REM L13 (20 DUPLICATES REMOVED)

=> d bib ab 1-
YOU HAVE REQUESTED DATA FROM 26 ANSWERS - CONTINUE? Y/(N):y

L14 ANSWER 1 OF 26 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 1
AN 2004:527503 CAPLUS
TI Telomere exchange between linear replicons of ***Borrelia*** burgdorferi
AU Huang, Wai Mun; Robertson, Margaret; Aron, John; ***Casjens, Sherwood***
CS Department of Pathology, University of Utah Medical School, Salt Lake City, UT, 84132, USA
SO Journal of Bacteriology (2004), 186(13), 4134-4141
CODEN: JOBAAY; ISSN: 0021-9193
PB American Society for Microbiology
DT Journal
LA English
AB Spirochetes in the genus ***Borrelia*** carry a linear chromosome and numerous linear plasmids that have covalently closed hairpin telomeres. The overall organization of the large chromosome of ***Borrelia*** burgdorferi appears to have been quite stable over recent evolutionary time; however, a large fraction of natural isolates carry differing lengths of DNA that extend the right end of the chromosome between about 7 and 20 kbp relative to the shortest chromosomes. We present evidence here that a rather recent nonhomologous recombination event in the B. burgdorferi strain Sh-2-82 lineage has replaced its right chromosomal telomere with a large portion of the linear plasmid lp21, which is present in the strain B31 lineage. At least two successive rounds of addn. of linear plasmid genetic material to the chromosomal right end appear to have occurred at the Sh-2-82 right telomere, suggesting that this is an evolutionary mechanism by which plasmid genetic material can become part of the chromosome. The unusual nonhomologous nature of this rearrangement suggests that, barring horizontal transfer, it can be used as a unique genetic marker for this lineage of B. burgdorferi chromosomes.
RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L14 ANSWER 2 OF 26 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
AN 2003:1039719 SCISEARCH
GA The Genuine Article (R) Number: 743TX
TI Bidirectional replication from an internal ori site of the linear N15 plasmid prophage
AU Ravin N V (Reprint); Kuprianov V V; Gilcrease E B; ***Casjens S R***
CS Russian Acad Sci, Ctr Bioengn, Prosp 60 Let Oktiabria, Bldg 7-1, Moscow 117312, Russia (Reprint); Russian Acad Sci, Ctr Bioengn, Moscow 117312, Russia; Univ Utah, Sch Med, Dept Pathol, Salt Lake City, UT 84132 USA
CYA Russia; USA
SO NUCLEIC ACIDS RESEARCH, (15 NOV 2003) Vol. 31, No. 22, pp. 6552-6560.
Publisher: OXFORD UNIV PRESS, GREAT CLARENDON ST, OXFORD OX2 6DP, ENGLAND.
ISSN: 0305-1048.
DT Article; Journal
LA English
REC Reference Count: 52
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The prophage of coliphage N15 is not integrated into the chromosome but exists as a linear plasmid molecule with covalently closed hairpin ends (telomeres). Upon infection the injected phage DNA circularizes via its cohesive ends. Then, a phage-encoded enzyme, protelomerase, cuts the circle and forms the hairpin telomeres. N15 protelomerase acts as a telomere-resolving enzyme during prophage DNA replication. We characterized the N15 replicon and found that replication of circular N15 miniplasmids requires only the repA gene, which encodes a multidomain protein homologous to replication proteins of bacterial plasmids replicated by a theta-mechanism. Replication of a linear N15 miniplasmid also requires the protelomerase gene and telomere regions. N15 prophage replication is initiated at an internal ori site located within repA and proceeds bidirectionally. Electron microscopy data suggest that after duplication of the left telomere, protelomerase cuts this site generating Y-shaped molecules. Full replication of the molecule and subsequent resolution of the right telomere then results in two linear plasmid molecules. N15 prophage replication thus appears to follow a mechanism that is distinct from that employed by eukaryotic replicons with this type of telomere and suggests the possibility of evolutionarily independent appearances of prokaryotic and eukaryotic replicons with covalently closed telomeres.

L14 ANSWER 3 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN DUPLICATE 2
AN 2003:223631 BIOSIS
DN PREV200300223631
TI Profiling of temperature-induced changes in ***Borrelia*** burgdorferi gene expression by using whole genome arrays.
AU Ojaimi, Caroline; Brooks, Chad; ***Casjens, Sherwood*** ; Rosa, Patricia; Elias, Abdallah; Barbour, Alan; Jasinskas, Algis; Benach, Jorge; Katona, Laura; Radolf, Justin; Caimano, Melissa; Skare, Jon; Swingle, Kristen; Akins, Darrin; Schwartz, Ira [Reprint Author]
CS Department of Microbiology and Immunology, New York Medical College, Valhalla, NY, 10595, USA
darrin-akins@ouhsc.edu; Schwartz@nymc.edu
SO Infection and Immunity, (April 2003) Vol. 71, No. 4, pp. 1689-1705. print. ISSN: 0019-9567 (ISSN print).
DT Article
LA English
ED Entered STN: 7 May 2003
Last Updated on STN: 7 May 2003
AB ***Borrelia*** burgdorferi is the etiologic agent of Lyme disease, the most prevalent arthropod-borne disease in the United States. The genome of the type strain, B31, consists of a 910,725-bp linear chromosome and 21 linear and circular plasmids comprising 610,694 bp. During its life cycle, the spirochete exists in distinctly different environments, cycling between a tick vector and a mammalian host. Temperature is one environmental factor known to affect B. burgdorferi gene expression. To identify temperature-responsive genes, genome arrays containing 1,662 putative B. burgdorferi open reading frames (ORFs) were prepared on nylon membranes and employed to assess gene expression in B. burgdorferi B31 grown at 23 and 35degreeC. Differences in expression of more than 3.5 orders of magnitude could be readily discerned and quantitated. At least minimal expression from 91% of the arrayed ORFs could be detected. A total of 215 ORFs were differentially expressed at the two temperatures; 133 were expressed at significantly greater levels at 35degreeC, and 82 were more significantly expressed at 23degreeC. Of these 215 ORFs, 134 are characterized as genes of unknown function. One hundred thirty-six (63%) of the differentially expressed genes are plasmid encoded. Of particular interest is plasmid lp54 which contains 76 annotated putative genes; 31 of these exhibit temperature-regulated expression. These findings underscore the important role plasmid-encoded genes may play in adjustment of B. burgdorferi to growth under diverse environmental conditions.

L14 ANSWER 4 OF 26 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 3
AN 2003:101209 CAPLUS

DN 138:349177
TI ***Borrelia*** burgdorferi gene expression profiling with membrane-based arrays
AU Ojaimi, Caroline; Brooks, Chad; Akins, Darrin; ***Casjens, Sherwood*** ; Rosa, Patricia; Elias, Abdallah; Barbour, Alan; Jasinskas, Algis; Benach, Jorge; Katonah, Laura; Radolf, Justin; Caimano, Melissa; Skare, Jon; Swingle, Kristen; Sims, Simon; Schwartz, Ira
CS Department of Microbiology and Immunology, New York Medical College, Valhalla, NY, 10595, USA
SO Methods in Enzymology (2002), 358(Bacterial Pathogenesis, Part C), 165-177
CODEN: MENZAU; ISSN: 0076-6879
PB Elsevier Science
DT Journal
LA English
AB A method to study ***Borrelia*** burgdorferi gene expression profiling with membrane-based arrays is described. Specifically, the methods contains prepn. of PCR-amplified open reading frames from B. burgdorferi strain B31 MI, the strain whose genome sequence has been elucidated, synthesis of labeled cDNA hybridization probe, hybridization, and statistical anal. about the obtained data.
RE.CNT 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L14 ANSWER 5 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2001:554148 BIOSIS
DN PREV200100554148
TI Bacteriophages of ***Borrelia*** burgdorferi and other spirochetes.
AU Eggers, Christian H. [Reprint author]; ***Casjens, Sherwood*** ; Samuels, D. Scott
CS Center for Microbial Pathogenesis, University of Connecticut Health Center, Farmington, CT, 06030, USA
SO Saier, Milton H., Jr. [Editor]; Garcia-Lara, Jorge [Editor]. (2001) pp. 35-44. JMMB Symposium Series. The spirochetes: Molecular and cellular biology. print.
Publisher: Horizon Scientific Press, 32 Hewitts Lane, Wymondham, Norfolk, NR18 0JA, UK. Series: JMMB Symposium Series.
ISBN: 1-898486-27-1 (cloth).
DT Book
Book; (Book Chapter)
LA English
ED Entered STN: 28 Nov 2001
Last Updated on STN: 25 Feb 2002

L14 ANSWER 6 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2001:553349 BIOSIS
DN PREV200100553349
TI ***Borrelia*** genomes.
AU ***Casjens, Sherwood*** [Reprint author]
CS Department of of Oncological Sciences, Division of Molecular Biology and Genetics, University of Utah, Salt Lake City, UT, 84132, USA
SO Saier, Milton H., Jr. [Editor]; Garcia-Lara, Jorge [Editor]. (2001) pp. 75-85. JMMB Symposium Series. The spirochetes: Molecular and cellular biology. print.
Publisher: Horizon Scientific Press, 32 Hewitts Lane, Wymondham, Norfolk, NR18 0JA, UK. Series: JMMB Symposium Series.
ISBN: 1-898486-27-1 (cloth).
DT Book
Book; (Book Chapter)
LA English
ED Entered STN: 28 Nov 2001
Last Updated on STN: 25 Feb 2002

L14 ANSWER 7 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 4
AN 2000:504125 BIOSIS
DN PREV200000504125
TI A second allele of eppA in ***Borrelia*** burgdorferi strain B31 is

located on the previously undetected circular plasmid cp9-2.
AU Miller, Jennifer C.; Bono, James L.; Babb, Kelly; El-Hage, Nazira; ***Casjens, Sherwood*** ; Stevenson, Brian [Reprint author]
CS Department of Microbiology and Immunology, University of Kentucky College of Medicine, Lexington, KY, 40536-0298, USA
SO Journal of Bacteriology, (November, 2000) Vol. 182, No. 21, pp. 6254-6258. print.
CODEN: JOBAAY. ISSN: 0021-9193.
DT Article
LA English
OS Genbank-AF213472
ED Entered STN: 22 Nov 2000
Last Updated on STN: 12 Feb 2002
AB Although sequence analysis of ***Borrelia*** burgdorferi isolate B31 was recently declared "complete," we found that cultures of this strain can contain a novel 9-kb circular plasmid, cp9-2. The newly described plasmid contains both sequence similarities with and differences from the previously identified B31 plasmid cp9-1 (formerly cp9). cp9-1 and cp9-2 each encode a unique allele of EppA, a putative membrane protein synthesized by B. burgdorferi during mammalian infection.

L14 ANSWER 8 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 5
AN 2000:254050 BIOSIS
DN PREV200000254050
TI Distribution of twelve linear extrachromosomal DNAs in natural isolates of lyme disease spirochetes.
AU Palmer, Nanette; Fraser, Claire; ***Casjens, Sherwood*** [Reprint author]
CS Department of Oncological Sciences, University of Utah Medical School, Salt Lake City, UT, 84132, USA
SO Journal of Bacteriology, (May, 2000) Vol. 182, No. 9, pp. 2476-2480. print.
CODEN: JOBAAY. ISSN: 0021-9193.
DT Article
LA English
ED Entered STN: 21 Jun 2000
Last Updated on STN: 5 Jan 2002
AB We have analyzed a panel of independent North American isolates of the Lyme disease agent spirochete, ***Borrelia*** burgdorferi (sensu stricto), for the presence of linear plasmids with sequence similarities to the 12 linear plasmids present in the B. burgdorferi type strain, isolate B31. The frequency of similarities to probes from each of the 12 B31 plasmids varied from 13 to 100% in the strain panel examined, and these similarities usually reside on plasmids similar in size to the cognate B31 plasmid. Sequences similar to 5 of the 12 B31 plasmids were found in all of the isolates examined, and >66% of the panel members hybridized to probes from 4 other plasmids. Sequences similar to most of the B. burgdorferi B31 plasmid-derived DNA probes used were also found on linear plasmids in the related Eurasian Lyme agents ***Borrelia*** garinii and ***Borrelia*** afzelii; however, some of these plasmids had uniform but substantially different sizes from their B. burgdorferi counterparts.

L14 ANSWER 9 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 6
AN 2000:123164 BIOSIS
DN PREV200000123164
TI A bacterial genome in flux: The twelve linear and nine circular extrachromosomal DNAs in an infectious isolate of the Lyme disease spirochete ***Borrelia*** burgdorferi.
AU ***Casjens, Sherwood*** [Reprint author]; Palmer, Nanette; van Vugt, Rene; Huang, Wai Mun; Stevenson, Brian; Rosa, Patricia; Lathigra, Raju; Sutton, Granger; Peterson, Jeremy; Dodson, Robert J.; Haft, Daniel; Hickey, Erin; Gwinn, Michelle; White, Owen; Fraser, Claire M.
CS Division of Molecular Biology and Genetics, Department of Oncological Sciences, University of Utah Medical School, Salt Lake City, UT, 84132,

USA
SO Molecular Microbiology, (Feb., 2000) Vol. 35, No. 3, pp. 490-516. print.
CODEN: MOMIEE. ISSN: 0950-382X.
DT Article
LA English
ED Entered STN: 5 Apr 2000
Last Updated on STN: 3 Jan 2002
AB We have determined that ***Borrelia*** burgdorferi strain B31 MI carries 21 extrachromosomal DNA elements, the largest number known for any bacterium. Among these are 12 linear and nine circular plasmids, whose sequences total 610 694 bp. We report here the nucleotide sequence of three linear and seven circular plasmids (comprising 290 546 bp) in this infectious isolate. This completes the genome sequencing project for this organism; its genome size is 1 521 419 bp (plus about 2000 bp of undetermined telomeric sequences). Analysis of the sequence implies that there has been extensive and sometimes rather recent DNA rearrangement among a number of the linear plasmids. Many of these events appear to have been mediated by recombinational processes that formed duplications. These many regions of similarity are reflected in the fact that most plasmid genes are members of one of the genome's 161 paralogous gene families; 107 of these gene families, which vary in size from two to 41 members, contain at least one plasmid gene. These rearrangements appear to have contributed to a surprisingly large number of apparently non-functional pseudogenes, a very unusual feature for a prokaryotic genome. The presence of these damaged genes suggests that some of the plasmids may be in a period of rapid evolution. The sequence predicts 535 plasmid genes gtoreq300 bp in length that may be intact and 167 apparently mutationally damaged and/or unexpressed genes (pseudogenes). The large majority, over 90%, of genes on these plasmids have no convincing similarity to genes outside ***Borrelia*** , suggesting that they perform specialized functions.

L14 ANSWER 10 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 7
AN 2002:140399 BIOSIS
DN PREV200200140399
TI The role of genomics in approaching the study of ***Borrelia*** DNA replication.
AU Garcia-Lara, Jorge [Reprint author]; Picardeau, Mathieu; Hinnebusch, B. Joseph; Huang, Wai Mun; ***Casjens, Sherwood***
CS Department of Microbiology, University of Georgia, 546 Biological Sciences Building, Athens, GA, 30602, USA
jgarcial@panda.uchc.edu
SO Journal of Molecular Microbiology and Biotechnology, (October, 2000) Vol. 2, No. 4, pp. 447-454. print.
ISSN: 1464-1801.
DT Article
General Review; (Literature Review)
LA English
ED Entered STN: 6 Feb 2002
Last Updated on STN: 26 Feb 2002
AB The identification of chromosomal and episomal origins of replication in the genome of the causative agent of Lyme disease, the spirochete ***Borrelia*** burgdorferi, has been greatly facilitated by genomics. Analysis of genome features, including strand compositional asymmetries, organizational similarities to other bacterial origins of replication, and the presence of homologues of genes involved in replication and partitioning, have contributed to the identification of a collection of putative origins of replication within the ***Borrelia*** genome. This analysis has provided the basis for the experimental verification of origins in the linear chromosome and in the linear plasmid lp28-2. Information generated during the study of these origins will significantly contribute to the understanding of the mechanisms of replication and partitioning in ***Borrelia*** .

L14 ANSWER 11 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 8

AN 2002:140393 BIOSIS
DN PREV200200140393
TI ***Borrelia*** genomes in the year 2000.
AU ***Casjens, Sherwood*** [Reprint author]
CS Department of Oncological Sciences, University of Utah Medical School, Salt Lake City, UT, 84132, USA
sherwood.casjens@hci.utah.edu
SO Journal of Molecular Microbiology and Biotechnology, (October, 2000) Vol. 2, No. 4, pp. 401-410. print.
ISSN: 1464-1801.
DT Article
General Review; (Literature Review)
LA English
ED Entered STN: 6 Feb 2002
Last Updated on STN: 26 Feb 2002
AB All analyzed members of the spirochete genus ***Borrelia*** contain a linear chromosome about 910 kbp long. The complete sequence of the B. burgdorferi B31 genome predicts that its chromosome carries essentially all of this organism's housekeeping genes. In accordance with these bacterial species' obligatory parasitic lifestyle, its genes encode enzymes that are capable of only a minimal metabolism, in which all nucleotides, amino acids, fatty acids and enzyme cofactors must be scavenged from the host. In addition to the chromosome, all ***Borrelia*** isolates examined carry multiple linear and circular plasmids with lengths between 5 and 200 kbp. The plasmids, which account for over 600 kbp in isolate B31, carry very few genes with homology to genes outside of the ***Borrelia*** genus. But they do carry numerous predicted lipoprotein genes, many of which are have been shown to be or are expected to be outer surface proteins. Ten of the linear plasmids have strikingly low protein coding potential for bacterial DNA. These plasmids have enjoyed numerous past duplicative rearrangements, which have resulted in the presence of a substantial fraction of the DNA that appears to be currently undergoing mutational decay, presumably because it is no longer under selection for function.

L14 ANSWER 12 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 9
AN 2002:140388 BIOSIS
DN PREV200200140388
TI Bacteriophages of spirochetes.
AU Eggers, Christian H.; ***Casjens, Sherwood*** ; Hayes, Stanley F.; Garon, Claude F.; Damman, Christopher J.; Oliver, Donald B.; Samuels, D. Scott [Reprint author]
CS Division of Biological Sciences, University of Montana, Missoula, MT, 59812, USA
samuels@selway.umt.edu
SO Journal of Molecular Microbiology and Biotechnology, (October, 2000) Vol. 2, No. 4, pp. 365-373. print.
ISSN: 1464-1801.
DT Article
General Review; (Literature Review)
LA English
ED Entered STN: 6 Feb 2002
Last Updated on STN: 26 Feb 2002
AB Historically, a number of bacteriophage-like particles have been observed in association with members of the bacterial order Spirochetales, the spirochetes. In the last decade, several spirochete bacteriophages have been isolated and characterized at the molecular level. We have recently characterized a bacteriophage of the Lyme disease agent, ***Borrelia*** burgdorferi, which we have designated variant phiBB-1. Here we review the history of the association between the spirochetes and their bacteriophages, with a particular emphasis on variant phiBB-1 and its prophage, the 32-kb circular plasmid family of B. burgdorferi.

L14 ANSWER 13 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2001:63185 BIOSIS
DN PREV200100063185

TI The unusual linear plasmids of the Lyme disease spirochete ***borrelia*** burgdorferi.
AU ***Casjens, S. R.*** [Reprint author]
CS Dept. of Oncological Sciences, U. of Utah Medical School, Salt Lake City, UT, 84132, USA
SO Biochemical Society Transactions, (October, 2000) Vol. 28, No. 5, pp. A102. print.
Meeting Info.: 18th International Congress of Biochemistry and Molecular Biology. Birmingham, UK. July 16-20, 2000. International Union of Biochemistry and Molecular Biology; Federation of European Biochemical Societies; Biochemical Society.
CODEN: BCSTB5. ISSN: 0300-5127.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 31 Jan 2001
Last Updated on STN: 12 Feb 2002

L14 ANSWER 14 OF 26 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1999:734795 CAPLUS
DN 132:90395
TI Evolution of the linear DNA replicons of the ***Borrelia*** spirochetes
AU ***Casjens, Sherwood***
CS Division of Molecular Biology and Genetics, Department of Oncological, University of Utah Medical School, Salt Lake City, UT, 84321, USA
SO Current Opinion in Microbiology (1999), 2(5), 529-534
CODEN: COMIF7; ISSN: 1369-5274
PB Current Biology Publications
DT Journal; General Review
LA English
AB A review with 59 refs. Members of the spirochete genus ***Borrelia*** carry numerous linear DNA replicons with covalently closed hairpin telomeres. The genome of one member of this genus, B. burgdorferi B31, has now been completely characterized and contains a linear chromosome, twelve linear plasmids and nine circular extra-chromosomal elements. The phylogenetic position of the ***Borrelia*** spirochetes strongly suggests that a progenitor with circular replicons acquired the ability to replicate linear DNA mols.
RE.CNT 59 THERE ARE 59 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L14 ANSWER 15 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1998:412591 BIOSIS
DN PREV199800412591
TI ***Borrelia*** burgdorferi and the other Lyme disease spirochetes.
AU ***Casjens, Sherwood*** ; Huang, Wai Mun
CS Dep. Oncol. Sci., Div. Mol. Biol. and Genet., Univ. Utah Health Sci. Cent., Salt Lake City, UT 84132, USA
SO de Bruijn, F. J. [Editor]; Lupski, J. R. [Editor]; Weinstock, G. M. [Editor]. (1998) pp. 621-624. Bacterial genomes: Physical structure and analysis. print.
Publisher: Chapman and Hall, Inc., 29 West 35th Street, New York, New York, USA; Chapman and Hall Ltd., 2-6 Boundary Row, London SE1 8HN, England.
ISBN: 0-412-99141-1.
DT Book
Book; (Book Chapter)
LA English
ED Entered STN: 2 Oct 1998
Last Updated on STN: 2 Oct 1998

L14 ANSWER 16 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 10
AN 1998:391139 BIOSIS
DN PREV199800391139
TI Evidence of past recombination events among the genes encoding the Erp

antigens of ***Borrelia*** burgdorferi.
AU Stevenson, Brian [Reprint author]; ***Casjens, Sherwood*** ; Rosa, Patricia
CS Dep. Microbiol. Immunol., MS 415 UKMC, Univ. Kentucky, Lexington, KY 40536, USA
SO Microbiology (Reading), (July, 1998) Vol. 144, No. 7, pp. 1869-1879. print.
ISSN: 1350-0872.
DT Article
LA English
OS Genbank-AF022479; Genbank-AF022480; Genbank-AF022481; Genbank-AF022482; Genbank-AF022483
ED Entered STN: 10 Sep 1998
Last Updated on STN: 10 Sep 1998
AB A single ***Borrelia*** burgdorferi bacterium may contain six or more different 32 kb circular plasmids (cp32s). Although these plasmids are homologous throughout much of their sequences, two loci have been identified at which they can vary significantly. The cp32 plasmids and their relatives each contain two adjacent genes, orfC and orf3, that vary in sequence between plasmids found within clones of individual bacteria. The orfC gene product is homologous to proteins involved in partitioning of bacterial plasmids, and the differences at this locus between plasmids may account for their compatibility. The orfC-orf3 loci are located approximately 5 kb from another variable locus called erp. The orfC-orf3 loci were used as physically linked markers to assess genetic rearrangements in the erp loci; this revealed examples of recombination involving both individual genes and entire erp loci. Recombination of the genes encoding the Erp antigens might contribute to the evasion of the mammalian immune response and could play roles in the establishment and persistence of B. burgdorferi infections in mammalian hosts.

L14 ANSWER 17 OF 26 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1997:778273 CAPLUS
DN 128:71459
TI ***Borrelia*** burgdorferi and the other Lyme disease spirochetes
AU ***Casjens, Sherwood*** ; Huang, Wai Mun
CS Department of Oncological Sciences Division of Molecular Biology & Genetics, University of Utah Health Science Center, Salt Lake City, UT, 84132, USA
SO Bacterial Genomes (1998), 621-624. Editor(s): De Bruijn, Frans J.; Lupski, James R.; Weinstock, George M. Publisher: Chapman & Hall, New York, N. Y.
CODEN: 65KVAK
DT Conference
LA English
AB The authors present phys. and genetic maps of ***Borrelia*** burgdorferi isolate Sh-2-82.
RE.CNT 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L14 ANSWER 18 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 11
AN 1997:344497 BIOSIS
DN PREV199799643700
TI Characterization of cp18, a naturally truncated member of the cp32 family of ***Borrelia*** burgdorferi plasmids.
AU Stevenson, Brian [Reprint author]; ***Casjens, Sherwood*** ; Van Vugt, Rene; Porcella, Stephen F.; Tilly, Kit; Bono, James L.; Rosa, Patricia
CS Lab. Microbial Structure Function, Rocky Mountain Lab., NIAID, NIH, 903 S. Fourth St., Hamilton, MT 59840, USA
SO Journal of Bacteriology, (1997) Vol. 179, No. 13, pp. 4285-4291.
CODEN: JOBAAY. ISSN: 0021-9193.
DT Article
LA English
ED Entered STN: 11 Aug 1997
Last Updated on STN: 11 Aug 1997
AB We have mapped the genes encoding the antigenic lipoproteins OspE and OspF

to an approximately 18-kb circular plasmid in ***Borrelia*** burgdorferi N40. Sequencing and restriction mapping have revealed that this plasmid, cp18, is homologous to an 18-kb region of the cp32 circular plasmids found in the Lyme disease spirochetes. Our data show that cp18 may have arisen from an ancestral cp32 plasmid by deletion of a 14-kb region of DNA, indicating that a significant portion of the cp32 plasmid is not essential in cis for plasmid maintenance. These findings suggest that a relatively small recombinant plasmid capable of being stably maintained in B. burgdorferi could be constructed from a cp32 plasmid.

L14 ANSWER 19 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 12
AN 1998:5384 BIOSIS
DN PREV199800005384
TI Telomeres of the linear chromosomes of Lyme disease spirochaetes: Nucleotide sequence and possible exchange with linear plasmid telomeres.
AU ***Casjens, Sherwood*** [Reprint author]; Murphy, Maria; Delange, Michael; Sampson, Laura; Vugt, Rene Van; Huang, Wai Mun
CS Div. Mol. Biol. Genet., Dep. Oncol. Sci., Univ. Utah Med. Sch., Salt Lake City, UT 84132, USA
SO Molecular Microbiology, (Nov., 1997) Vol. 26, No. 3, pp. 581-596. print. CODEN: MOMIEE. ISSN: 0950-382X.
DT Article
LA English
OS Genbank-AF08217; Genbank-AF08218; Genbank-AF08219
ED Entered STN: 23 Dec 1997
Last Updated on STN: 23 Dec 1997
AB Bacteria of the spirochaete genus ***Borrelia*** have linear chromosomes about 950 kbp in size. We report here that these linear chromosomes have covalently closed hairpin structures at their termini that are similar but not identical to those reported for linear plasmids carried by these organisms. Nucleotide sequence analysis of the chromosomal telomeric regions indicates that unique, apparently functional genes lie within a few hundred bp of each of the telomeres, and that there is an imperfect 26 bp inverted repeat at the two telomeres. In addition, we characterize a major chromosomal length polymorphism within the right telomeric regions of various ***Borrelia*** isolates, and show that sequences similar to those near the right telomere are often found on linear plasmids in B. burgdorferi (sensu stricto) isolates from nature. Sequences similar to a number of other regions of the chromosome, including those near the left telomere, were not found on B. burgdorferi plasmids. These observations suggest that there has been historical exchange of genetic information between the linear plasmids and the right end of the linear chromosome.

L14 ANSWER 20 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 13
AN 1998:46985 BIOSIS
DN PREV199800046985
TI Genomic sequence of a Lyme disease spirochaete, ***Borrelia*** burgdorferi.
AU Fraser, Claire M. [Reprint author]; ***Casjens, Sherwood*** ; Huang, Wai Mun; Sutton, Granger G.; Clayton, Rebecca; Lathigra, Raju; White, Owen; Ketchum, Karen A.; Dodson, Robert; Hickey, Erin K.; Gwinn, Michelle; Dougherty, Brian; Tomb, Jean-Francois; Fleischmann, Robert D.; Richardson, Delwood; Peterson, Jeremy; Kerlavage, Anthony R.; Quackenbush, John; Salzberg, Steven; Hanson, Mark; Van Vugt, Rene; Palmer, Nanette; Adams, Mark D.; Gocayne, Jeannine; Weidman, Janice; Utterback, Teresa; Watthey, Larry; McDonald, Lisa; Artiach, Patricia; Bowman, Cheryl; Garland, Stacey; Fujii, Claire; Cotton, Matthew D.; Horst, Kurt; Roberts, Kevin; Hatch, Bonnie; Smith, Hamilton O.; Venter, J. Craig
CS Inst. Genomic Res., 9712 Medical Center Drive, Rockville, MD 20850, USA
SO Nature (London), (Dec. 11, 1997) Vol. 390, No. 6660, pp. 580-586. print. CODEN: NATUAS. ISSN: 0028-0836.
DT Article
LA English
ED Entered STN: 27 Jan 1998

Last Updated on STN: 27 Jan 1998
AB The genome of the bacterium ***Borrelia*** burgdorferi B31, the aetiologic agent of Lyme disease, contains a linear chromosome of 910,725 base pairs and at least 17 linear and circular plasmids with a combined size of more than 533,000 base pairs. The chromosome contains 853 genes encoding a basic set of proteins for DNA replication, transcription, translation, solute transport and energy metabolism, but, like Mycoplasma genitalium, it contains no genes for cellular biosynthetic reactions. Because B. burgdorferi and M. genitalium are distantly related eubacteria, we suggest that their limited metabolic capacities reflect convergent evolution by gene loss from more metabolically competent progenitors. Of 430 genes on 11 plasmids, most have no known biological function; 39% of plasmid genes are paralogues that form 47 gene families. The biological significance of the multiple plasmid-encoded genes is not clear, although they may be involved in antigenic variation or immune evasion.

L14 ANSWER 21 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 14
AN 1997:438238 BIOSIS
DN PREV199799737441
TI The ***Borrelia*** burgdorferi circular plasmid cp26: Conservation of plasmid structure and targeted inactivation of the ospC gene.
AU Tilly, Kit [Reprint author]; ***Casjens, Sherwood*** ; Stevenson, Brian; Bono, James L.; Samuels, D. Scott; Hogan, Daniel; Rosa, Patricia
CS Lab. Microbial Structure Function, Natl. Inst. Allergy Infect. Dis., Rocky Mountain Lab., 903 S. 4th St., Hamilton, MT 59840, USA
SO Molecular Microbiology, (1997) Vol. 25, No. 2, pp. 361-373.
CODEN: MOMIEE. ISSN: 0950-382X.
DT Article
LA English
ED Entered STN: 8 Oct 1997
Last Updated on STN: 8 Oct 1997
AB The 26 to 28 kb circular plasmid of B. burgdorferi sensu lato (cp26) is ubiquitous among bacteria of this group and contains loci implicated in the mouse-tick transmission cycle. Restriction mapping and Southern hybridization indicated that the structure of cp26 is conserved among isolates from different origins and culture passage histories. The cp26 ospC gene encodes an outer surface protein whose synthesis within infected ticks increases when the ticks feed, and whose synthesis in culture increases after a temperature upshift. Previous studies of ospc coding sequences showed them to have stretches of sequence apparently derived from the ospC genes of distantly related isolates by homologous recombination after DNA transfer. We found conservation of the promoter regions of the ospC and guaA genes, which are divergently transcribed. We also demonstrated that the increase in OspC protein after a temperature upshift parallels increases in mRNA levels, as expected if regulatory regions adjoin the conserved sequences in the promoter regions. Finally, we used directed insertion to inactivate the ospC gene of a non-infectious isolate. This first example of directed gene inactivation in S. burgdorferi shows that the OspC protein is not required for stable maintenance of cp26 or growth in culture.

L14 ANSWER 22 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 15
AN 1997:86803 BIOSIS
DN PREV199799378516
TI Homology throughout the multiple 32-kilobase circular plasmids present in Lyme disease spirochetes.
AU ***Casjens, Sherwood*** [Reprint author]; Van Vugt, Rene; Tilly, Kit; Rosa, Patricia A.; Stevenson, Brian
CS Div. Mol. Biol. Genet., Dep. Oncol. Sci., Univ. Utah, Salt Lake City, UT 84132, USA
SO Journal of Bacteriology, (1997) Vol. 179, No. 1, pp. 217-227.
CODEN: JOBAAY. ISSN: 0021-9193.
DT Article
LA English
OS Genbank-U42598; Genbank-U44912; Genbank-U44913; Genbank-U44914;

Genbank-U60639; Genbank-U60640; Genbank-U60641; Genbank-U60642; Genbank-U60963; Genbank-U60964; Genbank-U60965; Genbank-U72996; Genbank-U72997; Genbank-U72998; Genbank-U72999; Genbank-U73000; Genbank-U73001

ED Entered STN: 26 Feb 1997
Last Updated on STN: 2 Apr 1997

AB We have characterized seven different 32-kb circular plasmids carried by ***Borrelia*** burgdorferi isolate B31. Restriction endonuclease recognition site mapping and partial sequencing of these plasmids indicated that all seven are probably closely related to each other throughout their lengths and have substantial relationships to cp8.3, an 8.3-kb circular plasmid of B. burgdorferi sensu lato isolate Ip21. With the addition of the seven 32-kb plasmids, this bacterial strain is known to carry at least 10 linear and 9 circular plasmids. Variant cultures of B. burgdorferi B31 lacking one or more of the 32-kb circular plasmids are viable and, at least in some cases, infectious. We have examined a number of different natural isolates of Lyme disease ***borreliae*** and found that all of the B. burgdorferi sensu stricto isolates and most of the B. burgdorferi sensu lato isolates tested appear to carry multiple 32-kb circular plasmids related to those of B. burgdorferi B31. The ubiquity of these plasmids suggests that they may be important in the natural life cycle of these organisms. They may be highly conjugative plasmids or prophage genomes, which could prove to be useful in genetically manipulating B. burgdorferi.

L14 ANSWER 23 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 16

AN 1996:537157 BIOSIS

DN PREV199699259513

TI Directed insertion of a selectable marker into a circular plasmid of ***Borrelia*** burgdorferi.

AU Rosa, Patricia [Reprint author]; Samuels, D. Scott; Hogan, Daniel; Stevenson, Brian; ***Casjens, Sherwood*** ; Tilly, Kit

CS Rocky Mountain Lab., 903 S. 4th St., Hamilton, MT 59840, USA

SO Journal of Bacteriology, (1996) Vol. 178, No. 20, pp. 5946-5953. CODEN: JOBAAY. ISSN: 0021-9193.

DT Article

LA English

ED Entered STN: 10 Dec 1996
Last Updated on STN: 10 Dec 1996

AB Studies of the biology of ***Borrelia*** burgdorferi and the pathogenesis of Lyme disease are severely limited by the current lack of genetic tools. As an initial step toward facile genetic manipulation of this pathogenic spirochete, we have investigated gene inactivation by allelic exchange using a mutated ***borrelial*** gyrB gene that confers resistance to the antibiotic coumermycin A-1 as a selectable marker. We have transformed B. burgdorferi by electroporation with a linear fragment of DNA in which this selectable marker was flanked by sequences from a native ***borrelial*** 26-kb circular plasmid. We have identified coumermycin A-1-resistant transformants in which gyrB had interrupted the targeted site on the 26-kb plasmid via homologous recombination with the flanking sequences. Antibiotic resistance conferred by the mutated gyrB gene on the plasmid is dominant, and transformed spirochetes carrying this plasmid do not contain any unaltered copies of the plasmid. Coumermycin A-1 resistance can be transferred to naive B. burgdorferi by transformation with ***borrelial*** plasmid DNA from the initial transformants. This work represents the first example of a directed mutation in B. burgdorferi whereby a large segment of heterologous DNA (gyrB) has been inserted via homologous recombination with flanking sequences, thus demonstrating the feasibility of specific gene inactivation by allelic exchange.

L14 ANSWER 24 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 17

AN 1996:331996 BIOSIS

DN PREV199699054352

TI Analysis of linear plasmid dimers in ***Borrelia*** burgdorferi sensu

lato isolates: Implications concerning the potential mechanisms of linear plasmid replication.
AU Marconi, Richard T. [Reprint author]; ***Casjens, Sherwood*** ; Munderloh, Ulrike G.; Samuels, D. Scott
CS Dep. Microbiol. Immunol., Med. Coll. Virginia, Virginia Commonwealth Univ., Richmand, VA 23298-0678, USA
SO Journal of Bacteriology, (1996) Vol. 178, No. 11, pp. 3357-3361. CODEN: JOBAAY. ISSN: 0021-9193.
DT Article
LA English
ED Entered STN: 26 Jul 1996
Last Updated on STN: 26 Jul 1996
AB The ***Borrelia*** genome is composed of a linear chromosome and a number of variable circular and linear plasmids. Atypically large linear plasmids of 92 to 105 kb have been identified in several ***Borrelia*** burgdorferi sensu lato isolates and characterized. These plasmids carry the p27 and ospAB genes, which in other isolates reside on a 50-kb plasmid. Here we demonstrate that these plasmids are dimers of the 50-kb ospAB plasmid (pAB50). The 94-kb plasmid from isolate VS116, pVS94, was an exception and did not hybridize with any plasmid gene probes. When this plasmid was used as a probe, homologous sequences in other isolates were not detected, suggesting that it is unique to isolate VS116. These analyses provide insight into the mechanism of linear plasmid replication and the mechanisms by which plasmid variability can arise.

L14 ANSWER 25 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 18
AN 1995:313474 BIOSIS
DN PREV199598327774
TI Linear Chromosomes of Lyme Disease Agent Spirochetes: Genetic Diversity and Conservation of Gene Order.
AU ***Casjens, Sherwood*** [Reprint author]; Delange, Michael; Leyi, Herbert L. Ii; Rosa, Patricia; Huang, Wai Mun
CS Dep. Oncol. Sci., Div. Mol. Biol. Genet., Univ. Utah Med. Cent., Salt Lake City, UT 84132, USA
SO Journal of Bacteriology, (1995) Vol. 177, No. 10, pp. 2769-2780. CODEN: JOBAAY. ISSN: 0021-9193.
DT Article
LA English
ED Entered STN: 30 Jul 1995
Last Updated on STN: 30 Jul 1995
AB We have constructed physical and genetic maps of the chromosomes of 21 Lyme disease agent spirochetes from geographically diverse locations. All have linear chromosomes whose lengths range from 935 to 955 kbp, and all contain multiple linear plasmids in the 16- to 175-kbp size range. The locations of 11 gene clusters on the chromosomes of these different isolates are indistinguishable at the resolution achieved in this study, indicating that the members of this related group of species have highly conserved chromosomal gene orders. However, chromosomal restriction endonuclease cleavage site maps are unique for nearly all isolates. The 22 chromosomal maps currently available define eight classes of Lyme disease agents. Four of these correspond to the previously proposed species ***Borrelia*** burgdorferi, ***Borrelia*** garinii, ***Borrelia*** afzelii, and ***Borrelia*** japonica. In addition, the North American isolates 21038, DN127 c19-2, 25015, and CA55 typify four additional chromosomal types that are as phylogenetically distinct as the species listed above. These findings support the idea that comparison of restriction maps is currently the most robust and definitive method for determining overall chromosomal relationships among closely related bacteria. In the course of this work, we located on the chromosome the previously unmapped outer surface protein-encoding LA7 gene and genes homologous to the Escherichia coli priA, plsC, parE, and parC genes, and we have substantially refined the locations of the recA, fla, p22A, and flgE genes.

L14 ANSWER 26 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 19

AN 1993:409251 BIOSIS
DN PREV199396074976
TI Linear chromosomal physical and genetic map of ***Borrelia*** burgdorferi, the Lyme disease agent.
AU ***Casjens, Sherwood*** [Reprint author]; Huang, Wai Mun
CS Dep. Cellular, Viral Molecular Biol., Univ. Utah Med. Cent., Salt Lake City, UT 84132, USA
SO Molecular Microbiology, (1993) Vol. 8, No. 5, pp. 967-980.
CODEN: MOMIEE. ISSN: 0950-382X.
DT Article
LA English
OS DDBJ-L12711; EMBL-L12711; Genbank-L12711
ED Entered STN: 8 Sep 1993
Last Updated on STN: 8 Sep 1993
AB A physical map of the 952 kbp chromosome of ***Borrelia*** burgdorferi Sh-2-82 has been constructed. Eighty-three intervals on the chromosome, defined by the cleavage sites of 15 restriction enzymes, are delineated. The intervals vary in size from 96 kbp to a few hundred bp, with an average size of 11.5 kbp. A striking feature of the map is its linearity; no other bacterial groups are known to have linear chromosomes. The two ends of the chromosome do not hybridize with one another, indicating that there are no large common terminal regions. The chromosome of this strain was found to be stable in culture; passage 6, 165 and 320 cultures have identical chromosomal restriction maps. We have positioned all previously known ***Borrelia*** burgdorferi chromosomal genes and several newly identified ones on this map. These include the gyrA/gyrB/dnaA/dnaN gene cluster, the rRNA gene cluster, fla, flgE, groEL (hsp60), recA, the rho/hip cluster, the dnak (hsp70)/dnaJ/grpE cluster, the pheT/pheS cluster, and the genes which encode the potent immunogen proteins p22A, p39 and p83. Our electrophoretic analysis detects five linear and at least two circular plasmids in B. burgdorferi Sh-2-82. We have constructed a physical map of the 53 kbp linear plasmid and located the operon that encodes the two major outer surface proteins ospA and opsB on this plasmid. Because of the absence of functional genetic tools for this organism, these maps will serve as a basis for future mapping, cloning and sequencing studies of B. burgdorferi.